

GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: April 25, 2005, 19:57:16 ; Search time 27.6718 Seconds  
(without alignments)  
834.495 Million cell updates/sec

Title: US-10-029-926d-235

Perfect score: 1266

Sequence: 1 MAEVQLVESGGGVRRPGSL.....RDSGNHVVGSGFTLVIG 240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	586	46.3	268	2 A56446	Ig heavy chain V r
2	588	44.9	109	2 S19663	Ig lambda chain V
3	562	44.4	108	2 S47184	Ig lambda chain -
4	561.5	44.4	249	2 S41374	single chain Fv an
5	551.5	43.6	110	2 S36272	Ig lambda chain V
6	546	43.1	127	2 S70444	Ig lambda chain pr
7	541	42.7	108	2 S38498	Ig lambda chain -
8	539	42.6	109	2 S38496	Ig lambda chain -
9	530	41.9	233	2 S25748	Ig lambda chain -
10	527	41.6	108	1 L3HUSH	Ig lambda chain V -
11	522.5	41.3	233	2 JCS322	p53 specific singl
12	518.5	41.0	110	2 S19672	Ig lambda chain V
13	517.5	40.9	146	2 S02083	Ig lambda chain V -
14	513	40.5	98	2 S26928	Ig heavy chain V r
15	510.5	40.3	128	2 S31595	Ig heavy chain V r
16	503	39.7	96	2 S36060	Ig lambda chain -
17	503	39.7	115	2 S13726	Ig lambda chain V
18	503	39.7	121	2 S31118	Ig heavy chain - h
19	502	39.7	123	2 S30532	Ig heavy chain V r
20	502	39.7	233	2 S25741	Ig lambda chain -
21	495.5	39.1	121	2 S31104	Ig heavy chain (su
22	495.5	39.1	112	2 PH1654	Ig heavy chain V r
23	491	38.8	120	2 S36273	Ig heavy chain V r
24	488	38.5	134	2 S31599	Ig heavy chain V r
25	487	38.5	138	2 S31566	Ig heavy chain V r
26	485.5	38.3	120	2 S44111	Ig heavy chain V-D
27	485.5	38.3	145	2 S11239	Ig heavy chain V r
28	485	38.3	119	2 S31108	Ig heavy chain - h
29	485	38.3	160	2 S05271	Ig heavy chain pre

30	484.5	38.3	120	2 S48798	Ig heavy chain V r
31	482	38.1	119	2 S31107	Ig heavy chain - h
32	480	37.9	121	2 I55673	Ig heavy chain - h
33	480	37.9	123	2 S31114	Ig heavy chain - h
34	478	37.8	119	2 D36005	Ig heavy chain V r
35	477	37.7	140	2 S31686	Ig heavy chain V r
36	476	37.6	119	2 C36005	Ig heavy chain V r
37	475	37.5	139	2 I37781	Ig variable region
38	473.5	37.4	124	2 S20782	Ig heavy chain V r
39	473.5	37.4	128	2 S26790	Ig heavy chain V r
40	473.5	37.4	140	2 S70442	Ig heavy chain pre
41	473.5	37.4	151	2 A60943	Ig heavy chain pre
42	473	37.4	127	2 S38489	Ig heavy chain - h
43	473	37.4	135	2 S31598	Ig heavy chain V r
44	472	37.3	98	2 S26927	Ig heavy chain V r
45	472	37.3	143	2 S23624	Ig heavy chain V r

#### ALIGNMENTS

##### RESULT 1

A56446 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996

C/Accession: A56446

R/Tang, P.M.; Folitz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident

A/Reference number: A56446; PMID:95229583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TRAN>

A/Cross-references: GB:U20617

C/Keywords: heterotetramer; immunoglobulin

Query Match 46.3%; Score 586; DB 2; Length 268;

Best Local Similarity 50.6%; Pred. No. 1.1e-33;

Matches 123; Conservative 34; Mismatches 78; Indels 8; Gaps 5;

Qy	1	MAEVQLVESGGGVRRPGSLRSCASGFTPDYGMWVRQAPKGLAEWVSINMNGST 60	
Db	1	MAOVKLQESGAEIVKFGASVLCSTTSGRNYKDTYHMKRPEQGLMIGRIAPANGIT 60	
Qy	61	GYADSVKGRFTISRDNKNSLYLQWNSLRPAEDTAVYYCAR---MRAPVIMGGCTLVTSR 117	
Db	61	KYDPRFGKATITADRTSSNTAVYQLSLTSEDTAVYYCASVYLTREYNTWGGCTTVTS 120	
Qy	118	GGGSGGGSGGGSGSS-ELTQDPAY-SVALGQTVRTTCGDSLRSYASWYQQKPGQAPV 175	
Db	121	GGGSGGGSGGGSGSDIELTQSPAIMSASLGEKVTMSCRASSSVN-FITWYQQKSDASP 179	
Qy	176	LVTVYSHMPSCGIPDFSSSGNTASLTITTAQAEDEADYVYCNSSDGNHVPFGGTR 235	
Db	180	LWVYTSHPGVPARFSGSGNSYSLTISMEGDAATYYCQPTSS--PTFSGTK 237	
Qy	236	LTV 238	
Db	238	LEI 240	

RESULT 2

S19663 Ig lambda chain V region (clone alpha-B5A3) - human

C/Species: Homo sapiens (man)

C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000

C/Accession: S19663

R/Mark, J.D.; Hoogenboom, H.R.; Bonnet, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991

A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage

A/Reference number: S19663; PMID:92085276; PMID:1748994

A/Accession: S19663  
 A/Molecule type: mRNA  
 A/Residues: 1-109 <MAR>  
 A/Cross-references: EMBL:X61640; NID:g29492; PIDN:CAA4821.1; PID:g1340166  
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F:15-89/Domain: immunoglobulin homology <IMV>

Query Match 44.9%; Score 568; DB 2; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-33;  
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 SSELTDPAVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLYYGNRPSGIPDR 191  
 Db 1 SSELTDPAVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLYYGNRPSGIPDR 60

QY 192 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLG 240  
 Db 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLG 109

## RESULT 3

S47184  
 Ig lambda chain - human  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C/Accession: S47184  
 R/McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.  
 Submitted to the EMBL Data Library, June 1994  
 A/Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient  
 A/Reference number: S47181  
 A/Accession: S47184  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-108 <MCI>  
 A/Cross-references: EMBL:X79783; NID:g506426; PIDN:CAA56179.1; PID:g506427  
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F:15-89/Domain: immunoglobulin homology <IMV>

Query Match 44.4%; Score 562; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 2e-32;  
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 SSELTDPAVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLYYGNRPSGIPDR 191  
 Db 1 SSELTDPAVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLYYGNRPSGIPDR 60

QY 192 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLG 239  
 Db 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLG 108

## RESULT 4

S41374  
 Single chain Fv antibody - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
 C/Accession: S41374  
 R/Atsessenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.  
 Submitted to the EMBL Data Library, January 1994  
 A/Description: Construction and functional characterization of a single chain Fv antibody  
 A/Reference number: S41374  
 A/Accession: S41374  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-249 <ART>  
 A/Cross-references: EMBL:Z29480

Query Match 44.4%; Score 561.5; DB 2; Length 249;  
 Best Local Similarity 48.6%; Pred. No. 5.2e-32;  
 Matches 121; Conservative 36; Mismatches 71; Indels 21; Gaps 6;

QY 3 EVQLVESGGGVRRPGGSLRLSCAASGFTPDYDGMSWVRQAPGKLEWISGIMNGSTGY 62  
 Db 1 QVLOQSGAEIVRRPGASVLTCTASGFNPKDYLIIHVKKRPERKLEWIRIAPASGNVXX 60

QY 63 AASVKRFTISDNMANSIYLOMNSLRADPTAVYCAR----MRAPVIGGGTLTVSRG 118  
 Db 61 VRRFDKATITVADTSSNTAVYLLSLTSDTAVYCARADTLVTSIGVYGQGSTVTVSSR 120

QY 119 GGGSGGGSGGGSS-ELTQD--PAVSVALGQTVRTTCQ-----GDSLSRYASWYQ 167  
 Db 121 GGGSGGGSGGGSDLELTQSPSVVYIPGESVISCRSSKALLYSDDGS----YLFWFL 176

QY 168 QKPGQAPVLYYGNRPSGIPDRFSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNH 227  
 Db 177 QKPGQAPVLYYGNRPSGIPDRFSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNH 234

## RESULT 5

S36272  
 Ig lambda chain V region (clone alpha-THY-29) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
 C/Accession: S36272  
 R/Giffiths, A.D.; Malmyvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
 EMBD J. 12, 725-734, 1993  
 A/Title: Human anti-self antibodies with high specificity from phage display libraries.  
 A/Reference number: S36256; MUID:93178448; PMID:7679990  
 A/Accession: S36272  
 A/Status: preliminary; nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1110 <GRI>  
 A/Cross-references: EMBL:Z18833; NID:g33419; PIDN:CAA79285.1; PID:g933912  
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F:15-89/Domain: immunoglobulin homology <IMV>

Query Match 43.6%; Score 551.5; DB 2; Length 110;  
 Best Local Similarity 98.2%; Pred. No. 1.1e-31;  
 Matches 108; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 132 SSELTDPAVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLYYGNRPSGIPDR 191  
 Db 1 SSELTDPAVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLYYGNRPSGIPDR 60

QY 192 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLG 240  
 Db 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLG 110

## RESULT 6

S70444  
 Ig lambda chain precursor V region - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
 C/Accession: S70444; S70426  
 R/Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.  
 Mol. Immunol. 29, 1363-1373, 1992  
 A/Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of B  
 A/Reference number: S70442; MUID:93024508; PMID:1383695  
 A/Accession: S70444  
 A/Status: not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-127 <CUI>  
 A/Cross-references: UNIPROT:Q9NSD6  
 A/Experimental source: clone E29.1  
 R/Tonnelle, C.  
 Submitted to the EMBL Data Library, May 1990  
 A/Reference number: S70426  
 A/Accession: S70426

Query Match 43.6%; Score 551.5; DB 2; Length 110;  
 Best Local Similarity 98.2%; Pred. No. 1.1e-31;  
 Matches 108; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

A:Molecule type: mRNA  
 A:Residues: 1-90 <TON>  
 A:Cross-references: EMBL:X53070  
 A:Experimental source: cell line E29.1, clone VL 29-1  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>  
 F:14-108/Domain: immunoglobulin homology <IMM>

Query Match 43.1%; Score 546; DB 2; Length 127;  
 Best Local Similarity 97.2%; Pred. No. 3e-31;  
 Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 132 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVYIGKNNRPSGIPDR 191  
 |||||  
 DB 20 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVYIGKNNRPSGIPDR 79

QY 192 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 239  
 |||||  
 DB 80 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 127

# RESULT 7

S38498  
 Ig lambda chain - human (fragment)

C:Species: Homo sapiens (man)  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C:Accession: S38498  
 R:Marx, J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.  
 submitted to the EMBL Data Library, June 1993  
 A:Description: Human antibody fragments specific for human blood group antigens from a F

A:Reference number: S38488  
 A:Accession: S38498  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-108 <MAR>

A:Cross-references: EMBL:Z23035; NID:g414043; PIDN:CAA80570.1; PID:g414044  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 42.7%; Score 541; DB 2; Length 108;  
 Best Local Similarity 97.2%; Pred. No. 5.7e-31;  
 Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 133 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVYIGKNNRPSGIPDR 192  
 |||||  
 DB 1 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVYIGKNNRPSGIPDR 60

QY 193 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 240  
 |||||  
 DB 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 108

# RESULT 8

S38496  
 Ig lambda chain - human (fragment)

C:Species: Homo sapiens (man)  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C:Accession: S38496  
 R:Marx, J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.  
 submitted to the EMBL Data Library, June 1993  
 A:Description: Human antibody fragments specific for human blood group antigens from a F

A:Reference number: S38488  
 A:Accession: S38496  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-109 <MAR>

A:Cross-references: EMBL:Z23031; NID:g414039; PIDN:CAA80566.1; PID:g414040  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 42.6%; Score 539; DB 2; Length 109;  
 Best Local Similarity 93.6%; Pred. No. 7.9e-31;  
 Matches 102; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 132 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVYIGKNNRPSGIPDR 191  
 |||||  
 DB 1 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVYIGKNNRPSGIPDR 60

QY 192 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 240  
 |||||  
 DB 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 109

# RESULT 9

S25748  
 Ig lambda chain - human

C:Species: Homo sapiens (man)  
 C>Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C:Accession: S25748  
 R:Combracio, G.; Klobbeck, H.G.  
 Eur. J. Immunol. 21, 1513-1522, 1991  
 A:Title: V(Lambda) and J(Lambda) gene segments of the human immunoglobulin la

A:Reference number: S16439; NID:91257162; PMID:1904362  
 A:Accession: S25748  
 A:Status: preliminary; translation not shown

A:Molecule type: mRNA  
 A:Residues: 1-233 <COM>  
 A:Cross-references: EMBL:X57813; NID:g33725; PIDN:CAA40950.1; PID:g33726  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 41.9%; Score 530; DB 2; Length 233;  
 Best Local Similarity 91.7%; Pred. No. 7.3e-30;  
 Matches 100; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 132 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVYIGKNNRPSGIPDR 191  
 |||||  
 DB 20 SSELTDPAVVALGQTVRITTCGDSLRSYASWYQKPGQAPVLVYIGKNNRPSGIPDR 79

QY 192 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 240  
 |||||  
 DB 80 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTYLTVLG 128

# RESULT 10

L3HUSH  
 Ig lambda chain V-III region (Sh) - human

C:Species: Homo sapiens (man)  
 C>Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004  
 C:Accession: A01980  
 R:Tilanti, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.  
 J. Biol. Chem. 245, 2171-2176, 1970

A:Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The complete

A:Reference number: A92057; NID:70166723; PMID:4909564  
 A:Accession: A01980  
 A:Molecule type: protein  
 A:Residues: 1-108 <TIT>  
 A:Cross-references: UNIPROT:P01714  
 A>Note: the sequence of the C region is also given

C:Genetic: GDB:IGLV6  
 A:Gene: GDB:IGLV6  
 A:Cross-references: GDB:119342; OMIM:147240  
 A:Map position: 22q11.2-22q11.2  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k  
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:14-88/Domain: immunoglobulin homology <IMM>  
 F:21-86/Disulfide bonds: #status experimental

Query Match 41.6%; Score 527; DB 1; Length 108;







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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:10:00 ; Search time 123.991 Seconds

(without alignments)  
991.192 Million cell updates/sec

Title: US-10-029-926D-235

Perfect score: 1266

Sequence: 1 MAEVLVSGGVGVRPGSL.....RDSGNHVVRGGSTKLTVLG 240

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	758	59.9	240	2	065ZC9
2	715	56.5	255	2	06KBO5
3	695.5	54.9	248	2	065ZD7
4	691.5	54.6	258	2	09QYF0
5	636	50.2	244	2	065ZC8
6	600	47.4	241	2	0921A6
7	578	45.7	243	2	07TQW2
8	552	43.6	107	2	09NSD5
9	550.5	43.5	112	2	09HCT1
10	548	43.3	487	2	065ZL2
11	530	41.9	233	2	06GMM4
12	527	41.6	108	1	LV3A_HUMAN
13	512	40.4	472	2	06N0B9
14	510	40.3	489	2	08NSK4
15	507.5	40.1	218	2	0925S1
16	504	39.8	173	2	08WJ38
17	483	38.2	121	2	09UL71
18	476	37.6	470	2	06PJ44
19	476	37.6	478	2	06PI81
20	476	37.6	606	2	06GMV2
21	472	37.4	613	2	08WUK1
22	472.5	37.3	597	2	096BB9
23	472	37.3	464	2	06MZU6
24	470	37.1	113	2	09UL90
25	465.5	36.8	473	2	06GMV2
26	464	36.7	493	2	06GMV2
27	461.5	36.5	118	2	09UL91
28	456.5	36.1	475	2	06MZU6
29	455	35.9	466	2	06IN78
30	452.5	35.7	479	2	06MZV6
31	446.5	35.3	116	1	HV3T_HUMAN

32	444.5	35.1	122	1	HV3G_HUMAN
33	444	35.1	116	2	09UL93
34	444	35.1	473	2	091Z05
35	442.5	35.0	465	2	06P6C4
36	442	34.9	117	1	HV3C_HUMAN
37	440.5	34.8	494	2	096K68
38	438.5	34.6	483	2	06MZX9
39	438.5	34.6	494	2	06ZW64
40	438.5	34.6	544	2	06PJ95
41	438	34.6	479	2	091WP5
42	436.5	34.5	118	2	09UL72
43	436.5	34.5	475	2	06GMV7
44	434	34.3	233	2	08TBC9
45	434	34.3	480	2	06N094

## ALIGNMENTS

## RESULT 1

ID	Q65ZC9	PRELIMINARY;	PRT;	240 AA.
AC	Q65ZC9;			
DT	25-OCT-2004 (TREMBL)	28, Created		
DT	25-OCT-2004 (TREMBL)	28, Last sequence update		
DT	25-OCT-2004 (TREMBL)	28, Last annotation update		
DE	Single-chain Fv (Fragment).			
GN	Name=scrFv;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C1q/7;			
RX	MEDLINE=97362799; PubMed=9219263;			
RA	Kontermann R.B., Wing M.G., Winter G.;			
RT	"Complement recruitment using bispecific diabodies";			
RL	Nat. Biotechnol. 15:629-631(1997).			
DR	EMBL; Y13056; CAJ73499.1; --			
DR	InterPro; IPR003599; Ig_			
DR	InterPro; IPR007110; Ig_1ike.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig; 2.			
DR	SMART; SM00409; Ig; 2.			
DR	SMART; SM00406; Ig; 2.			
DR	PROSITE; PS50835; Ig_LIKE; 2.			
FT	NON_TER 1			
FT	NON_TER 240			
SQ	SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;			

Query Match 59.9%; Score 758; DB 2; Length 240;  
Best Local Similarity 62.9%; Pred. No. 5.7e-48;  
Matches 151; Conservative 32; Mismatches 51; Indels 6; Gaps 4;

QY	3	EVOLVSGGVVRPGSLRISCAASGFTPDYGSWVRQAPGKLEAVSGINNGSGTGY 62
DB	1	QVDLVOSGGGLVOPGSLRISCAASGFTFSYGHWVRQAPGKLEAVVAISTDGSNKYY 60
QY	63	ADSVKGRFTTSPNNAKSLYLQNMNLSRAEDTAVVYCARMAPVI--NGOGTLVTVSRGGG 120
DB	61	ADSVKGRFTTSPNNAKSLYLQNMNLSRAEDTAVVYCARMDGSLDIPGKGTITLVVSSGGG 120
QY	121	GSGGGSGGGGGG-ELTQDPA-VSVALGQTVRTTCGDSLRSTYASVYQKPGQAPLVVI 178
DB	121	GSGGGSGGGGGGSDIOWTQSPSTISASIGDVTTCRASEGIIYVLAWYQKPGAPLVLI 180
QY	179	YGNKNRPSGLPDRFSSGSSGNTASLTITGAQADEADYVGNRDSGNHVVRGGSTLTV 238
DB	181	YKASLSLRAPSRPSGSGSTDTTLTISLQPDPAITVC--QQSYNYPILPFGGTLLEI 238



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Db      38 MAQVKLQSGGGLVKPKGSLKLSCAASGSDPSRYMMSWVRQAPKGLWIGELINPDSTI 97
Qy      61 GYADSVKGRFTISRDNKNSLYLQNMISLRADPTAVVYCARMR---APVIMGGTTLTVSR 117
Db      98 NTPSLKDKFIIISRDNKNSLYLQNMISLRADPTAVVYCARMR---APVIMGGTTLTVSR 157
Qy      118 GGGGGGGGGGGGGGGSS-ELTQDPA-VSVALGQTVRITTCQDLSRSYASWYQOKPGQAPV 175
Db      158 GGGGGGGGGGGGGGGSS-ELTQDPA-VSVALGQTVRITTCQDLSRSYASWYQOKPGQAPV 217
Qy      176 LVYIKGNRRPBGIPDRPFGSSSGNTASLTGQAQAEADYCNRSRDSGNH----VVF 230
Db      218 LVVYNAKTLADGVPSPRFGSGSGTQYSLKINSIQPEDFGSYCC-----QHPWTPPYTF 270
Qy      231 GGGTTLTV 238
Db      271 GGGTTLTV 278

RESULT 5
065ZC8      PRELIMINARY;      PRT;      244 AA.
ID 065ZC8;
AC 065ZC8;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scfv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
FT SEQUENCE FROM N.A.
SQ MEDLINE=97362799; PubMed=9219263;
RX Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13057; CAA73500.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17668338F2BF CRC64;

Query Match 50.2%; Score 636; DB 2; Length 244;
Best Local Similarity 50.8%; Pred. No. 5.3e-39;
Matches 124; Conservative 46; Mismatches 64; Indels 10; Gaps 4;

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RESULT 6
0921A6      PRELIMINARY;      PRT;      241 AA.
ID 0921A6;
AC 0921A6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
FT SEQUENCE FROM N.A.
SQ MEDLINE=98170165; PubMed=9509426;
RX Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
generation of a single-chain Fv molecule (scfv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -.
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.
DR PIR; S26325; S26325.
DR HSSP; P01607; IBMW.
DR SMART; SM00406; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 47.4%; Score 600; DB 2; Length 241;
Best Local Similarity 51.9%; Pred. No. 2.3e-36;
Matches 126; Conservative 34; Mismatches 67; Indels 16; Gaps 6;

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Qy      3 EVOLVSGGGVVRPGGSLRLSCAASGFTPDYGMVSRQAPGKLEWVSGINNGSTGY 62
Db      1 QVQLVSGAEVKKPQGGVKSCAKSGYTTSDHMHWRQAPGQGLEWGMGIDPNNQDTRF 60
Qy      63 ADSVKGRFTISRDNKNSLYLQNMISLRADPTAVVYCAR---MRAPVIMGGTTLTVS 116
Db      61 AQRFQGRVMTTRDTISAAAYMEVSRISRSDTAVYYCARBETGSAIYGMQDVGQGLTVVS 120
Qy      117 RGGGGGGGGGGGGSS-ELTQDPA-VSVALGQTVRITTCQDLSRSYASWYQOKPGQAP 174
Db      121 SGGGGGGGGGGGGSS-ELTQDPA-VSVALGQTVRITTCQDLSRSYASWYQOKPGQAP 180
Qy      175 VLVIYGNRRPBGIPDRPFGSSSGNTASLTGQAQAEADYCNRSRDSGNHVVFGGTF 234
Db      181 KPLIYKASLSASGAPRFRFGSGSGTDFLTITSLQPDPAFYIC--QQYSNPLTGGGT 238
Qy      235 KLTIV 238
Db      239 KLEI 242

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RESULT 7
07TQM2      PRELIMINARY;      PRT;      243 AA.
ID 07TQM2;
AC 07TQM2;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE scFv 6H8 protein (Fragment).
GN Name=scfv 6H8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;

```

RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Balb/C;  
 RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;  
 RA Peter U.C.; Eftekhari P.; Billiald P.; Wallukat G.; Hoebeke U.;  
 RT "scfv single chain antibody variable fragment as inverse agonist for  
 the beta-2 adrenergic receptor";  
 RL J. Biol. Chem. 278:36740-36747(2003).  
 DR EMBL: AJ574851; CA00495.1; -.  
 DR HSSP: P01751; 1A6W  
 DR InterPro: IPR007110; Ig-like.  
 DR SMART; SM00406; IGV; 2.  
 DR PROSITE; PSS0835; IG\_LIKE; 2.  
 FT NON TER 1  
 SQ SEQUENCE 243 AA; 25976 MW; BEFF642DDCF4F76 CRC64;

Query Match 45.7%; Score 578; DB 2; Length 243;  
 Best Local Similarity 49.4%; Pred. No. 9.6e-35;  
 Matches 118; Conservative 37; Mismatches 78; Indels 6; Gaps 4;

QY 3 EVOLVSGGAVNPGSLRSCASGFTPDYMSWRQAPGKLEWVGINNCGSTGY 62  
 DB 1 QVQLQSGSELPVPGASVKLSCKASGFTFTYTHWYKQRHGGGLEWIGNIVFGSGITNY 60  
 QY 63 ADSVGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAR-MRAPIVWGQGLTVYVRSGGG 121  
 DB 61 DEFKKKGILTVDTSSSTAAMHLSLASEDSAVYYCARGRGLDWAGATTLTVSSGGG 120  
 QY 122 SGGGSGGGGSS-ELTQ-DPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIY 179  
 DB 121 SGGGSGGGGSDIQMTQSSSFVSLGDRVLTICKASEDIYNRLAWYQKPGNAPRLIS 180  
 QY 180 GKNNRPGIDPRSGSSGNTASLTITGAQAEADYVYCNRSNGHVFEGGTGLTV 238  
 DB 181 GATSLGTGVSRRSGSGSDYTLTSLQTEDEVATYVYCOQYWSTR--TFGGGTLEI 236

## RESULT 8

QNSND6 PRELIMINARY; PRT; 107 AA.  
 AC QNSND6;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Homo sapiens This CDS feature is included to show the translation of  
 the corresponding V-region. Presently translation qualifiers on  
 DE V-region features are illegal. (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymphocyte;  
 RA Hohmann A.;  
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: LA4092; AAA69746.2; -.  
 DR FJR; S70444; S70444.  
 DR HSSP; P01709; 2MCG.  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON TER 1  
 FT NON TER 107  
 SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 43.6%; Score 552; DB 2; Length 107;  
 Best Local Similarity 98.1%; Pred. No. 3.2e-33;  
 Matches 105; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 134 ELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIDPRFS 193

DB 1 ELTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIDPRFS 60  
 QY 194 GSSSGNTASLTITGAQAEADYVYCNRSNGHVFEGGTGLTVLG 240  
 DB 61 GSSSGNTASLTITGAQAEADYVYCNRSNGHVFEGGTGLTVLG 107

## RESULT 9

QNSHCC1 PRELIMINARY; PRT; 112 AA.  
 AC QNSHCC1;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Single chain Fv (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Kikuchi M.; Takeda C.; Teujimoto Y.; Asada S.; Nagata K.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB049915; BAB16829.1; -.  
 DR HSSP; P01783; 1IGC.  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON TER 1  
 FT NON TER 112  
 SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 43.5%; Score 550.5; DB 2; Length 112;  
 Best Local Similarity 94.6%; Pred. No. 4.3e-33;  
 Matches 106; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 3 EVOLVSGGAVNPGSLRSCASGFTPDYMSWRQAPGKLEWVGINNCGSTGY 62  
 DB 1 EVOLVSGGAVNPGSLRSCASGFTPDYMSWRQAPGKLEWVGINNCGSTGY 60  
 QY 63 ADSVGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAR-MRAPIVWGQGLTV 113  
 DB 61 ADSVGRFTISRDNANKSLYLQNNSLRAEDTAVYYCARRYALDYWGQGLTV 112

## RESULT 10

Q652L2 PRELIMINARY; PRT; 487 AA.  
 AC Q652L2;  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 DE Fv/M4.  
 GN Name=M4-IFN-<tau>;  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10095;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96272580; PubMed=8688499;  
 RA Qi Y.; Xiang J.;  
 RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric  
 antibody secreted from myeloma cells.";  
 RL Hum. Antibodies Hybridomas 6:161-166(1995).  
 DR EMBL; S82493; AAB37424.2; -.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR003006; Ig\_MHC.

DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF07654; Cl-sec; 2.  
 DR GO: GO:000447; Ig; 4.  
 DR SMART: SM00409; Ig; 3.  
 DR SMART: SM00407; Ig; 3.  
 DR SMART: SM00408; Ig; 2.  
 DR SMART: SM00406; Ig; 2.  
 DR PROSITE: PS00835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
 DR PROSITE: 487 AA; 53578 MW; C7BAB69F30555504 CRC64;  
 SO SEQUENCE

Query Match 43.3%; Score 548; DB 2; Length 487;  
 Best Local Similarity 45.6%; Pred. No. 3.3e-32;  
 Matches 109; Conservative 45; Mismatches 79; Indels 6; Gaps 5;

QY 2 AEVQLVESGGGVVPRPGSGLRLSCAASGFTPDYGMISVRAPKGLKLEWVGIMNGSGTG 61  
 DB 19 SQVQLQDSDELVPKPAVSVKISCKASGYTFTDHAHNAKQKPGQGLEWIGYISPGNDIK 78  
 QY 62 YADSVAGRFITSHDNNAKSLYLQMNSLRAEDTAVVYCARMRAPVIMQGTLYTVSRGGG 121  
 DB 79 YNKKFKGKXLTLDKSSSTMYQLNLSLSDSAVPEKSYG-HMGQGITLIGS-GGGG 136  
 QY 122 SGGSGSGGGSS-ELTQDPA-VSVALGQTVRTTCGDSLRSYASWYQKPGAPLVLY 179  
 DB 137 SGGSGSGGGSSRIQMTQSPASISVAGELVITCRASENITYSLAWYQKQKSPQLLY 196  
 QY 180 GKNNRSGIPDRSSSGSGTASLTITGAQAEDEADYVYCNRSRSGNHVFGGKTLTV 238  
 DB 197 AATNLADGVSRSPSGSGSGTQYSLKINSLSQSEDFGSGY--QHFWGTPYTFGGTTRLEI 253

RESULT 11  
 OEGM4 PRELIMINARY; PRT; 233 AA.  
 AC 06GMA4;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grose L.H., Derge J.G.,  
 RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hulten F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Millay S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,  
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grumet J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywicki M.I., Skalska U., Smaluk D.E., Schmech A., Schein J.E.,  
 RA Jones S.J., Matra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC073786; AAH73786.1; -  
 DR GO: GO:0005489; P.election transporter activity; IEA.  
 DR GO: GO:0006118; P.election transport; IEA.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig-cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR InterPro: IPR006662; Thioed.  
 DR Pfam: PF07654; Cl-sec; 1.  
 DR Pfam: PF00047; Ig; 2.  
 DR PRINTS: PR00421; THIOREDOXIN.  
 DR SMART: SM00409; Ig; 2.  
 DR SMART: SM00407; Ig; 1.  
 DR SMART: SM00406; Ig; 1.  
 DR PROSITE: PS00835; IG\_LIKE; 2.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
 DR Hypothetical protein.  
 SO SEQUENCE 233 AA; 24855 MW; 46267783B8FDE5BD CRC64;

Query Match 41.9%; Score 530; DB 2; Length 233;  
 Best Local Similarity 91.7%; Pred. No. 3.1e-31;  
 Matches 100; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 132 SSELTDPAVSVALGQTVRTTCGDSLRSYASWYQKPGAPLVLYGKNNRPSGIPDR 191  
 DB 20 SSELTDPAVSVALGQTVRTTCGDSLRTTYASWYQKPGAPLVLYADNRPFGVPR 79  
 QY 192 FSGSSSGNTASLTITGAQAEDEADYVYCNRSRSGNHVFGGKTLTVLG 240  
 DB 80 FSGSGSGNTASLTITGAQAEDEADYVYCNRSRSGSHLVFGTGTQVTVLG 128

RESULT 12  
 LV3A HUMAN STANDARD; PRT; 108 AA.  
 AC P01714;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig lambda chain V-III region SH.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE=70166723; PubMed=4909564;  
 RA Titani K., Wikler M., Shinoda T., Putnam F.W.;  
 RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The  
 complete amino acid sequence and the location of the disulfide  
 bridges.";  
 RL J. Biol. Chem. 245:2171-2176(1970).  
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.  
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 DR PIR: A01980; 13HUSH.  
 DR HSSP: P01703; 7FAB.  
 DR GO: GO:0005576; C:extracellular; NAS.  
 DR GO: GO:0003823; F:antigen binding; NAS.  
 DR GO: GO:0006955; P:immune response; NAS.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; Ig; 1.  
 DR PROSITE: PS00835; IG\_LIKE; 1.  
 KM Bence-Jones protein; Direct protein sequencing;  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 97 Ig-like.  
 FT DISULFID 21 86  
 FT NON\_TER 108  
 SO SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;

Query Match 41.6%; Score 527; DB 1; Length 108;





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ID Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR HSSP; P01665; IONZ.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 40.1%; Score 507.5; DB 2; Length 218;
Best Local Similarity 47.7%; Pred. No. 1.3e-29;
Matches 102; Conservative 38; Mismatches 65; Indels 9; Gaps 4;

QY 1 MAEVOLVESGGGVVRPGSLRLSCAASGFTEDDYGMGWRQAPGKGLGWVSGINMGST 60
DB 1 MAQVKLQSGPELKKFEETVRISCKASGYFTTAGMQWVQKMPGKGLKWIWINTHSGVP 60
QY 61 GYADSVKGRFTISRDNKNSLYLQMNSLRADPTAVVYCARMAP--VINGGTLVTVSR 117
DB 61 KYAEFFKGRFAFLFETASATAYLIQISNLKNEDEATVFCMRMDYDGGFAVWGQGTIVTVSS 120
QY 118 GGGGGGGGGGGGGGGSS-ELTQDPA-VSVALGQTVRITCG---DSLRSYYASWYQKPG 171
DB 121 GGGGGGGGGGGGGGGSDIVLTQSPASLAVSLGQRATISCRASESVDNIGISFNNWFOOKPG 180
QY 172 QAPVLVIYCKNNRPSGIPDRFGSSSGNTASLTI 205
DB 181 QPPKLIIYASKQSGVPAGLASGSGTDFSLNI 214

```

Search completed: April 25, 2005, 20:34:05  
 Job time : 124.991 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 25, 2005, 19:56:06 ; Search time 3.06541 Seconds  
(without alignments)  
630.846 Million cell updates/sec

Title: US-10-029-926D-114

Perfect score: 28  
Sequence: 1 DYGMS 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	5	3 AAY95191	AAY95191 Anti-Plat
2	28	100.0	5	5 ABG78239	ABG78239 Human Fv
3	28	100.0	5	5 ABG91930	ABG91930 Human ant
4	28	100.0	5	6 ABU11271	ABU11271 Human TAN
5	28	100.0	5	8 ADI28371	ADI28371 Human CDR
6	28	100.0	10	7 ADM07746	ADM07746 Canine im
7	28	100.0	13	7 ADM75761	ADM75761 Potential
8	28	100.0	13	7 ADM75496	ADM75496 Potential
9	28	100.0	13	7 ADM75231	ADM75231 Potential
10	28	100.0	13	7 ADM75760	ADM75760 Potential
11	28	100.0	13	7 ADM74966	ADM74966 Potential
12	28	100.0	13	7 ADM74967	ADM74967 Potential
13	28	100.0	14	8 ABM79481	ABM79481 Human Fac
14	28	100.0	16	2 AAR49460	AAR49460 Factor VI
15	28	100.0	20	5 ABJ05002	ABJ05002 A3 peptid
16	28	100.0	26	1 AAF61435	AAF61435 Factor VI
17	28	100.0	29	1 AAP50314	AAP50314 Peptide e
18	28	100.0	33	1 AAP50318	AAP50318 Peptide e
19	28	100.0	41	1 AAP50313	AAP50313 Thrombin
20	28	100.0	60	5 AAB04948	AAB04948 A3 domain
21	28	100.0	73	3 AAB07206	AAB07206 Human Fac
22	28	100.0	98	3 AAB40073	AAB40073 Anti-H1L1
23	28	100.0	98	5 ABG78186	ABG78186 Human Fv
24	28	100.0	98	5 ABG91877	ABG91877 Human ant
25	28	100.0	98	6 ABO27087	ABO27087 Human ger

26	28	100.0	98	7 ADP09916	ADP09916 Antibody
27	28	100.0	98	7 ADP10126	ADP10126 Antibody
28	28	100.0	98	7 ADP10024	ADP10024 VEGF anti
29	28	100.0	98	7 ADJ80300	ADJ80300 VH gene 1
30	28	100.0	113	3 AAY95177	AAY95177 Anti-Plat
31	28	100.0	113	3 AAY95178	AAY95178 Anti-Plat
32	28	100.0	115	3 AAY95189	AAY95189 Anti-Plat
33	28	100.0	115	3 AAY95190	AAY95190 Anti-Plat
34	28	100.0	116	2 AAM19880	AAM19880 CEA-speci
35	28	100.0	117	2 AAR66312	AAR66312 Human imm
36	28	100.0	118	4 AAU02560	AAU02560 Anti-adip
37	28	100.0	120	2 AAR25204	AAR25204 OP-G2 mon
38	28	100.0	123	8 ADJ57861	ADJ57861 Light var
39	28	100.0	207	5 AAU98019	AAU98019 Human ace
40	28	100.0	211	1 AAP50091	AAP50091 Truncated
41	28	100.0	211	3 AAB07203	AAB07203 Human Fac
42	28	100.0	214	3 AAG38412	AAG38412 Arabidops
43	28	100.0	232	7 ABO62069	ABO62069 Klebsiell
44	28	100.0	235	8 ADR28086	ADR28086 NPB polyp
45	28	100.0	236	3 AAG29486	AAG29486 Arabidops

## ALIGNMENTS

RESULT 1  
ID AAY95191 standard; peptide; 5 AA.  
AC AAY95191;  
DT 29-AUG-2000 (first entry)  
XX  
DE Anti-platelet glycoprotein IB human H1B-1 VH CDR1.  
XX  
KW Variable heavy chain; single chain antibody; scFv; human; H1B-1;  
KW glycoprotein IB alpha; platelet; aggregation; antiaggregant;  
KW antithrombotic; thrombus; therapy; diagnostic; CDR1;  
KW complementarity determining region.  
XX  
OS Homo sapiens.  
XX  
PN WO200026667-A1.  
PD 11-MAY-2000.  
XX  
PF 29-OCT-1999; 99WO-US025495.  
PR 30-OCT-1998; 98US-0106275P.  
XX  
PA (MILLER) MILLER J L.  
XX  
PI MILLER JL;  
DR WPI; 2000-365744/31.  
XX  
PT Isolated nucleic acid molecule encoding anti-human platelet glycoprotein  
PT IB alpha molecule useful for producing antibodies which inhibit platelet  
PT aggregation.  
XX  
PS Claim 14; Fig 5; 89pp; English.  
XX  
CC The present sequence is that of complementarity determining region 1  
CC (CDR1) of the heavy chain variable region (VH) of human single chain  
CC antibody (scFv) H1B-1 (see AAY95198), which is directed against platelet  
CC glycoprotein IB (GP1b). The H1B series of scFv was isolated from a human  
CC synthetic VH and VL scFv library on the basis of their binding to  
CC platelet GP1b. Whether displayed as surface proteins on a phagemid or  
CC secreted as free scFv by *Escherichia coli*, the H1B scFv clones are  
CC capable of inhibiting von Willebrand factor-dependent aggregation of  
CC platelets. The scFv are composed of native human protein sequences and  
CC are therefore attractive potential reagents for therapeutic purposes.  
CC They provide a new class of antithrombotic agents, useful for the

CC prevention of platelet-dependent thrombi in diseased arteries, bypass  
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.  
 CC Methods of inhibiting aggregation of platelets, of binding human platelet  
 CC GPIIb/IIIa and of selecting a VH or VL region of an antibody that  
 CC inhibits platelet aggregation are claimed. Fragments of the scFv VH or VL  
 CC chain, including CDR fragments, are also claimed

XX Sequence 5 AA;

Query Match 100.0%; Score 28; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
 |||||  
 DB 1 DYGMS 5

RESULT 2

ID ABG78239 standard; peptide; 5 AA.

AC ABG78239;

DT 15-NOV-2002 (first entry)

XX Human Fv molecule hypervariable region related peptide #114.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;

KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

OS Homo sapiens.

EN WO200259264-A2.

PD 01-AUG-2002.

PF 31-DEC-2001; 2001WO-US049440.

PR 29-DEC-2000; 2000US-00751181.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

PA Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

PI Plakstein D, Peretz T;

DR WPI; 2002-619166/66.

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 PT or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favor of other  
 PT cells.

PS Claim 20; Page 208; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has actively against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention

XX Sequence 5 AA;

Query Match 100.0%; Score 28; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
 |||||  
 DB 1 DYGMS 5

RESULT 3

ID ABG91930 standard; peptide; 5 AA.

AC ABG91930;

DT 04-DEC-2002 (first entry)

XX Human antibody fragment #114.

XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;

KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
 KM myocardial infarction; retinopathic disease; abnormal platelet function;  
 KM sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.

EN WO200253700-A2.

PD 11-JUL-2002.

PF 31-DEC-2001; 2001WO-US049442.

PR 29-DEC-2000; 2000US-00751181.

PR 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

PA Lazarovits J, Hagai Y, Plakstein D, Vogel T, Nimrod A, Mar-Haim H;

PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

DR WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer.

PS Claim 25; Page 284; 0pp; English.

XX The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility  
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia  
 CC cells in a patient, or in the manufacture of a medicament for the above  
 CC mentioned purposes. The epitopes are useful for diagnosing and treating  
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
 CC diseases, cardiovascular diseases such as myocardial infarction,  
 CC retinopathic diseases and other diseases mediated by abnormal platelet  
 CC function and diseases caused by sulphated tyrosine-dependent protein-  
 CC protein interactions. This sequence represents a human antibody fragment  
 CC of the invention

XX

SQ Sequence 5 AA;  
 Query Match 100.0%; Score 28; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
 |||||  
 DB 1 DYGMS 5

RESULT 4  
 ABU1271  
 ID ABU1271 standard; peptide; 5 AA.  
 XX  
 AC ABU1271;  
 DT 06-FEB-2003 (first entry)  
 DE Human TANGO 268 VHCDR1 Peptide #5.  
 XX  
 KM Human; mouse; variable heavy; VH; antigen; cancer;  
 KM complementarity determining region; TANGO 268; glycoprotein VI; GPII;  
 KM TANGO 268; extracellular matrix; collagen; platelet release;  
 KM proliferation; migration; embryogenesis; inflammation; thrombosis;  
 KM degranulation; thrombocytopenia; antibody; thrombotic disorder;  
 KM cerebral vascular disease; stroke; ischemia; venous thromboembolism;  
 KM leg swelling; pain; ulceration; pulmonary embolism; coronary disease;  
 KM cardiovascular disease; angina pectoris; myocardial infarction;  
 KM coronary stenosis; atherosclerosis; immunological disorder;  
 KM developmental disorder; embryonic disorder; liver disorder;  
 KM cerebral vascular disease; venous thromboembolism disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200280968-A1.  
 PD 17-OCT-2002.  
 XX  
 PF 09-APR-2002; 2002WO-US011122.  
 XX  
 PR 09-APR-2001; 2001US-00829495.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 PI Bugfield SJ, Villeva J, Jandrot-Perrus M, Vainchenker W;  
 PI Gill DS, Qian DM, Kingsbury G;  
 PI  
 DR WPI; 2003-058477/05.  
 XX  
 PT Novel substantially purified antibody immunospecifically binding to TANGO  
 PT 268 antigen, useful for treating bleeding disorders such as  
 PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.  
 XX  
 PS Claim 1; Page 11; 236pp; English.

This invention relates to a novel purified antibody comprising a variable  
 heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;  
 or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically  
 binding to a TANGO 268 (also referred as glycoprotein VI (GPII)) antigen.  
 The antibodies of the invention act to decrease or block TANGO 268  
 binding to extracellular matrix components, or as a Collagen or platelet  
 release and aggregation blocker. The antibodies of the invention are  
 useful for modulating proliferation, migration, morphology,  
 differentiation and/or function of megakaryocytes and platelets,  
 including during development e.g. embryogenesis, modulating leukocyte-  
 platelet and platelet-endothelium interactions in inflammation and/or  
 thrombosis, and modulating platelet aggregation and degranulation. They  
 are also useful for modulating disorders associated with abnormal or  
 aberrant megakaryocyte and/or platelet proliferation, migration,  
 morphology, differentiation and/or function, e.g. bleeding disorders such  
 as thrombocytopenia. Other diseases which may be modulated by these  
 antibodies are thrombotic disorders, cerebral vascular diseases (e.g.

CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases  
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);  
 CC coronary diseases (e.g. cardiovascular diseases including angina  
 CC pectoris, myocardial infarction, coronary stenosis, atherosclerosis,  
 CC etc); immunological disorders, developmental disorders, embryonic  
 CC disorders, liver disorders, cerebral vascular diseases, venous  
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The  
 CC antibodies of the invention only causes a transient decrease in platelet  
 CC counts, platelet aggregation, and/or platelet activation and so have some  
 CC advantages over prior art methods. The present sequence represents a  
 CC peptide sequence used to generate the antibodies of the invention  
 XX

SQ Sequence 5 AA;  
 Query Match 100.0%; Score 28; DB 6; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
 |||||  
 DB 1 DYGMS 5

RESULT 5  
 ADI28371  
 ID ADI28371 standard; peptide; 5 AA.  
 XX  
 AC ADI28371;  
 DT 06-MAY-2004 (first entry)  
 DE Human CDR1 peptide, used in therapeutic composition.  
 XX  
 KM Human; antibody; scFv; complementarity determining region; drug delivery;  
 KM cancer; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004002528-A1.  
 PD 08-JAN-2004.  
 XX  
 PF 30-JUN-2003; 2003WO-US020604.  
 XX  
 PR 01-JUL-2002; 2002US-00189025.  
 PA (SAVI-) SAVIENT PHARM INC.  
 PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;  
 PI  
 DR WPI; 2004-099189/10.  
 XX  
 PT Composition comprising an agent and/or antibody or its fragment, useful  
 PT for treating auto-immune disease, thrombosis, stenosis, metastasis, or  
 PT for inhibiting growth and/or replication of tumor cells or leukemia  
 PT cells.  
 XX  
 PS Claim 15; SEQ ID NO 6; 56pp; English.

The present sequence is that of a human antibody complementarity  
 determining region 1 (CDR1). The invention relates to compositions  
 utilizing an agent and an antibody or its fragment. The agent is a toxin,  
 radioisotope or pharmaceutical agent such as doxorubicin. It is complexed  
 CC or combined with or conjugated to the antibody or its fragment. The  
 CC antibody may have a first hypervariable region comprising a CDR3, a  
 CC second hypervariable region comprising a CDR2 and a third hypervariable  
 CC sequence comprising the present CDR1 sequence. The agent and/or antibody  
 CC can be present in the composition is a sub-clinical amount, i.e. less  
 CC than the amount generally found to be clinically effective when the agent  
 CC is administered alone. The composition is used in claimed methods of:  
 CC inhibiting cell rolling, inflammation, thrombosis, restenosis,  
 CC metastasis, the growth and/or replication of tumor cells or leukaemia  
 CC cells, an increase in number of tumour or leukaemia cells, cell-cell,

CC cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet  
 CC complex formation, aggregation or adhesion; increasing the mortality rate  
 CC of tumour or leukaemia cells, the susceptibility of disease cells to  
 CC damage by anti-disease agents, and the susceptibility of tumour or  
 CC leukaemia cells to damage by anti-cancer agents; and ameliorating the  
 CC effects of a disease, preventing a disease, treating a disease or  
 CC inhibiting the progress of a disease.

XX  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 28; DB 8; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYGM5 5  
 |||||  
 Db 1 DYGM5 5

RESULT 6

ADM07746  
 ID ADM07746 standard; peptide; 10 AA.

XX  
 AC ADM07746;

XX  
 DT 20-MAY-2004 (first entry)

XX  
 DE Canine immunoglobulin heavy chain variable domain CDR1 peptide 14.

XX  
 KW canine; dog; heavy; immunoglobulin; antibody light chain variable domain;

KW antiallergic; allergy; IgE; gene therapy;  
 KW complementarity determining region; CDR1.

XX  
 OS Canis familiaris.

XX  
 PN WO2003060080-A2.

XX  
 PD 24-JUL-2003.

XX  
 PF 20-DEC-2002; 2002WO-US041362.

XX  
 PR 21-DEC-2001; 2001US-0344874P.

XX  
 PA (IDEXX-) IDEXX LAB INC.

PI Krah ER, Guo H, Aiyappa A, Lawton R;

DR WPI; 2003-598521/56.

XX  
 PT New canine heavy and light chain variable domain polypeptides, useful for  
 PT treating canine allergy.

XX  
 PS Claim 15; Page 95; 130pp; English.

XX  
 CC The invention relates to a novel canine heavy or light chain variable  
 CC domain polypeptide. The protein of the invention demonstrates

CC antiallergic activity and may be useful for treating canine allergy,  
 CC possibly via gene therapy. The current sequence is that of a canine

CC immunoglobulin heavy chain variable domain complementarity determining  
 CC region (CDR) peptide of the invention.

XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 28; DB 7; Length 10;

Best Local Similarity 100.0%; Pred. No. 9.2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYGM5 5  
 |||||  
 Db 6 DYGM5 10

RESULT 7

ADM75761  
 ID ADM75761 standard; peptide; 13 AA.

XX  
 AC ADM75761;

XX  
 DT 03-JUN-2004 (first entry)

XX  
 DE Potential human MHC class II binding human Factor VIII peptide #981.

XX  
 KW human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;  
 KW MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.

XX  
 OS Homo sapiens.

XX  
 PN WO2003087161-A1.

XX  
 PD 23-OCT-2003.

XX  
 PF 17-APR-2003; 2003WO-EP04063.

XX  
 PR 18-APR-2002; 2002EP-00008712.

XX  
 PR 24-MAR-2003; 2003EP-00006554.

XX  
 PA (MERE) MERCK PATENT GMBH.

XX  
 PI Jones T, Baker M, Carr FJ;

XX  
 DT WPI; 2003-845307/78.

XX  
 PT New modified human Factor VIII molecule being substantially non-  
 PT immunogenic or less immunogenic than non-modified human Factor VIII,  
 PT useful in preparing a composition for treating e.g., Gaucher's disease.

XX  
 PS Disclosure; Fig 1; 68pp; English.

XX  
 CC The invention relates to a novel modified human Factor VIII molecule. The  
 CC modified human Factor VIII molecule being substantially non-immunogenic

CC or less immunogenic than a non-modified human Factor VIII and having  
 CC essentially the same biological specificity and activity when used in

CC vivo. The modified human Factor VIII molecule comprises specifically  
 CC altered amino acid residues compared with the non-modified parental

CC molecule, where the altered amino acid residues cause a reduction or an  
 CC elimination of one or more of the T-cell epitopes, which act in the

CC parental non-modified molecule as MHC class II binding ligands and  
 CC stimulate T-cells. The potential MHC class II binding activity peptide is

CC useful for the manufacture of the modified Factor VIII molecule or a  
 CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.

CC The modified Factor VIII molecule is useful in preparing a composition  
 CC for treating e.g., Gaucher's disease. This sequence represents a human

CC Factor VIII peptide with potential human MHC class II binding activity of  
 CC the invention.

XX  
 SQ Sequence 13 AA;

Query Match 100.0%; Score 28; DB 7; Length 13;

Best Local Similarity 100.0%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYGM5 5  
 |||||  
 Db 3 DYGM5 7

RESULT 8

ADM75496  
 ID ADM75496 standard; peptide; 13 AA.

XX  
 AC ADM75496;

XX  
 DT 03-JUN-2004 (first entry)

XX  
 DE Potential human MHC class II binding human Factor VIII peptide #716.

KW human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;  
 KM MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003087161-A1.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 17-APR-2003; 2003WO-EP004063.  
 XX  
 PR 18-APR-2002; 2002EP-00008712.  
 PR 24-MAR-2003; 2003EP-00006554.  
 XX  
 PA (MERE ) MERCK PATENT GMBH.  
 XX  
 PI Jones T, Baker M, Carr FJ;  
 DR WPI; 2003-845307/78.  
 XX  
 PT New modified human Factor VIII molecule being substantially non-  
 immunogenic or less immunogenic than non-modified human Factor VIII,  
 useful in preparing a composition for treating e.g., Gaucher's disease.  
 XX  
 PS Disclosure; Fig 1; 68pp; English.  
 XX  
 CC The invention relates to a novel modified human Factor VIII molecule. The  
 modified human Factor VIII molecule being substantially non-immunogenic  
 or less immunogenic than a non-modified human Factor VIII and having  
 essentially the same biological specificity and activity when used in  
 vivo. The modified human Factor VIII molecule comprises specifically  
 altered amino acid residues compared with the non-modified parental  
 molecule, where the altered amino acid residues cause a reduction or an  
 elimination of one or more of the T-cell epitopes, which act in the  
 parental non-modified molecule as MHC class II binding ligands and  
 stimulate T-cells. The potential MHC class II binding activity peptide is  
 useful for the manufacture of the modified Factor VIII molecule or a  
 vaccine in order to reduce immunogenicity to Factor VIII in a patient.  
 CC The modified Factor VIII molecule is useful in preparing a composition  
 for treating e.g., Gaucher's disease. This sequence represents a human  
 Factor VIII peptide with potential human MHC class II binding activity of  
 the invention.  
 CC  
 CC  
 SQ Sequence 13 AA;  
 XX  
 Query Match 100.0%; Score 28; DB 7; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYGMS 5  
 |||||  
 DB 4 DYGMS 8  
 XX  
 RESULT 9  
 ADM75231  
 ID ADM75231 standard; peptide; 13 AA.  
 XX  
 AC ADM75231;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Potential human MHC class II binding human Factor VIII peptide #451.  
 XX  
 KM human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;  
 KM MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003087161-A1.  
 XX  
 PD 23-OCT-2003.  
 XX

PF 17-APR-2003; 2003WO-EP004063.  
 XX  
 PR 18-APR-2002; 2002EP-00008712.  
 PR 24-MAR-2003; 2003EP-00006554.  
 XX  
 PA (MERE ) MERCK PATENT GMBH.  
 XX  
 PI Jones T, Baker M, Carr FJ;  
 DR WPI; 2003-845307/78.  
 XX  
 PT New modified human Factor VIII molecule being substantially non-  
 immunogenic or less immunogenic than non-modified human Factor VIII,  
 useful in preparing a composition for treating e.g., Gaucher's disease.  
 XX  
 PS Disclosure; Fig 1; 68pp; English.  
 XX  
 CC The invention relates to a novel modified human Factor VIII molecule. The  
 modified human Factor VIII molecule being substantially non-immunogenic  
 or less immunogenic than a non-modified human Factor VIII and having  
 essentially the same biological specificity and activity when used in  
 vivo. The modified human Factor VIII molecule comprises specifically  
 altered amino acid residues compared with the non-modified parental  
 molecule, where the altered amino acid residues cause a reduction or an  
 elimination of one or more of the T-cell epitopes, which act in the  
 parental non-modified molecule as MHC class II binding ligands and  
 stimulate T-cells. The potential MHC class II binding activity peptide is  
 useful for the manufacture of the modified Factor VIII molecule or a  
 vaccine in order to reduce immunogenicity to Factor VIII in a patient.  
 CC The modified Factor VIII molecule is useful in preparing a composition  
 for treating e.g., Gaucher's disease. This sequence represents a human  
 Factor VIII peptide with potential human MHC class II binding activity of  
 the invention.  
 CC  
 CC  
 SQ Sequence 13 AA;  
 XX  
 Query Match 100.0%; Score 28; DB 7; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYGMS 5  
 |||||  
 DB 5 DYGMS 9  
 XX  
 RESULT 10  
 ADM75760  
 ID ADM75760 standard; peptide; 13 AA.  
 XX  
 AC ADM75760;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Potential human MHC class II binding human Factor VIII peptide #980.  
 XX  
 KM human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;  
 KM MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003087161-A1.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 17-APR-2003; 2003WO-EP004063.  
 XX  
 PR 18-APR-2002; 2002EP-00008712.  
 PR 24-MAR-2003; 2003EP-00006554.  
 XX  
 PA (MERE ) MERCK PATENT GMBH.  
 XX  
 PI Jones T, Baker M, Carr FJ;  
 XX

DR WPI; 2003-845307/78.  
XX New modified human Factor VIII molecule being substantially non-  
PT immunogenic or less immunogenic than non-modified human Factor VIII,  
PT useful in preparing a composition for treating e.g., Gaucher's disease.  
XX  
XX Disclosure; Fig 1; 68pp; English.  
XX  
CC The invention relates to a novel modified human Factor VIII molecule. The  
CC modified human Factor VIII molecule being substantially non-immunogenic  
CC or less immunogenic than a non-modified human Factor VIII and having  
CC essentially the same biological specificity and activity when used in  
CC vivo. The modified human Factor VIII molecule comprises specifically  
CC altered amino acid residues compared with the non-modified parental  
CC molecule, where the altered amino acid residues cause a reduction or an  
CC elimination of one or more of the T-cell epitopes, which act in the  
CC parental non-modified molecule as MHC class II binding ligands and  
CC stimulate T-cells. The potential MHC class II binding activity peptide is  
CC useful for the manufacture of the modified Factor VIII molecule or a  
CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.  
CC The modified Factor VIII molecule is useful in preparing a composition  
CC for treating e.g., Gaucher's disease. This sequence represents a human  
CC Factor VIII peptide with potential human MHC class II binding activity of  
CC the invention.  
XX  
SQ Sequence 13 AA;  
XX  
Query Match 100.0%; Score 28; DB 7; Length 13;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYGMS 5  
DB 9 DYGMS 13  
XX  
RESULT 11  
ADM74966  
ID ADM74966 standard; peptide; 13 AA.  
XX  
XX ADM74966;  
AC  
DT 03-JUN-2004 (first entry)  
XX  
DE Potential human MHC class II binding human Factor VIII peptide #186.  
XX  
KM human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;  
KM MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.  
XX  
OS Homo sapiens.  
OS  
PN WO2003087161-A1.  
XX  
PD 23-OCT-2003.  
XX  
PF 17-APR-2003; 2003WO-EP004063.  
XX  
PR 18-APR-2002; 2002EP-00008712.  
PR 24-MAR-2003; 2003EP-00006554.  
XX  
PA (MERCK ) MERCK PATENT GMBH.  
XX  
PI Jones T, Baker M, Carr FJ;  
XX  
DR WPI; 2003-845307/78.  
XX  
XX New modified human Factor VIII molecule being substantially non-  
PT immunogenic or less immunogenic than non-modified human Factor VIII,  
PT useful in preparing a composition for treating e.g., Gaucher's disease.  
XX  
XX Disclosure; Fig 1; 68pp; English.  
XX  
CC The invention relates to a novel modified human Factor VIII molecule. The

CC modified human Factor VIII molecule being substantially non-immunogenic  
CC or less immunogenic than a non-modified human Factor VIII and having  
CC essentially the same biological specificity and activity when used in  
CC vivo. The modified human Factor VIII molecule comprises specifically  
CC altered amino acid residues compared with the non-modified parental  
CC molecule, where the altered amino acid residues cause a reduction or an  
CC elimination of one or more of the T-cell epitopes, which act in the  
CC parental non-modified molecule as MHC class II binding ligands and  
CC stimulate T-cells. The potential MHC class II binding activity peptide is  
CC useful for the manufacture of the modified Factor VIII molecule or a  
CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.  
CC The modified Factor VIII molecule is useful in preparing a composition  
CC for treating e.g., Gaucher's disease. This sequence represents a human  
CC Factor VIII peptide with potential human MHC class II binding activity of  
CC the invention.  
XX  
SQ Sequence 13 AA;  
XX  
Query Match 100.0%; Score 28; DB 7; Length 13;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYGMS 5  
DB 8 DYGMS 12  
XX  
RESULT 12  
ADM74967  
ID ADM74967 standard; peptide; 13 AA.  
XX  
XX ADM74967;  
AC  
DT 03-JUN-2004 (first entry)  
XX  
DE Potential human MHC class II binding human Factor VIII peptide #187.  
XX  
KM human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;  
KM MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.  
XX  
OS Homo sapiens.  
OS  
PN WO2003087161-A1.  
XX  
PD 23-OCT-2003.  
XX  
PF 17-APR-2003; 2003WO-EP004063.  
XX  
PR 18-APR-2002; 2002EP-00008712.  
PR 24-MAR-2003; 2003EP-00006554.  
XX  
PA (MERCK ) MERCK PATENT GMBH.  
XX  
PI Jones T, Baker M, Carr FJ;  
XX  
DR WPI; 2003-845307/78.  
XX  
XX New modified human Factor VIII molecule being substantially non-  
PT immunogenic or less immunogenic than non-modified human Factor VIII,  
PT useful in preparing a composition for treating e.g., Gaucher's disease.  
XX  
XX Disclosure; Fig 1; 68pp; English.  
XX  
CC The invention relates to a novel modified human Factor VIII molecule. The  
CC modified human Factor VIII molecule being substantially non-immunogenic  
CC or less immunogenic than a non-modified human Factor VIII and having  
CC essentially the same biological specificity and activity when used in  
CC vivo. The modified human Factor VIII molecule comprises specifically  
CC altered amino acid residues compared with the non-modified parental  
CC molecule, where the altered amino acid residues cause a reduction or an  
CC elimination of one or more of the T-cell epitopes, which act in the  
CC parental non-modified molecule as MHC class II binding ligands and  
CC stimulate T-cells. The potential MHC class II binding activity peptide is



CC useful for the manufacture of the modified Factor VIII molecule or a  
CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.  
CC The modified Factor VIII molecule is useful in preparing a composition  
CC for treating e.g., Gaucher's disease. This sequence represents a human  
CC Factor VIII peptide with potential human MHC class II binding activity of  
CC the invention.  
CC  
XX

XX Sequence 13 AA;

Query Match 100.0%; Score 28; DB 7; Length 13;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
| | | | |  
DB 2 DYGMS 6

#### RESULT 13

ABM79481  
ID ABM79481 standard; peptide; 14 AA.

XX ABM79481;

XX 22-APR-2004 (first entry)

DE Human Factor VIII peptide fragment SEQ ID NO: 5.

XX Antibody; human; Factor VIII; LRP; haemostatic; haemophilia A;

KM low-density lipoprotein receptor-related protein;

KM blood coagulation disorder.

XX Homo sapiens.

XX WO2003093313-A2.

XX 13-NOV-2003.

XX 28-APR-2003; 2003WO-EP004425.

XX 29-APR-2002; 2002US-0376351P.

XX (BAXT ) BAXTER INT INC.

XX (BAXT ) BAXTER HEALTHCARE SA.

XX (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.

XX Mertens K, Bovenschen AN, Voorberg J, Rieger M, Scheiflinger F;

XX WPI; 2004-053039/05.

XX Use of peptides derived from and antibodies generated against Factor VIII

XX to inhibit Factor VIII interaction with Low Density Lipoprotein Receptor

XX protein or to prevent or treat blood coagulation disorders (e.g.

XX hemophilia A).

XX Example 1; Page 49; Opp; English.

XX The present invention relates to peptides derived from Factor VIII but

XX not having any substantial Factor VIII activity, or an antibody which

XX specifically binds to epitopes within the amino acid sequences, which can

XX be used to inhibit Factor VIII interaction with Low Density Lipoprotein

XX Receptor Protein (LRP). The peptides or antibody are useful in inhibiting

XX Factor VIII interaction with LRP, in decreasing Factor VIII degradation

XX in a biological fluid, in prolonging Factor VIII half-life in blood or in

XX preparing a medicament for preventing or treating a blood coagulation

XX disorder (e.g. haemophilia A or von Willebrand's disease) and/or a

XX temporary impairment of the thrombolytic or fibrinolytic systems. The

XX present sequence is a polypeptide shown in the exemplification of the

XX invention

XX Sequence 14 AA;

XX Query Match 100.0%; Score 28; DB 8; Length 14;

Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
| | | | |  
DB 2 DYGMS 6

#### RESULT 14

AAR49460  
ID AAR49460 standard; protein; 16 AA.

XX AAR49460;

XX 25-MAR-2003 (revised)

DT 16-SEP-1994 (first entry)

DE Factor VIII position 1175-1790.

XX Naturally-occurring; immunomodulatory protein; human; therapy; class I;

KM major histocompatibility complex; class II; allotype; type I diabetes;

KM autoimmune disease; rheumatoid arthritis; T-cell-mediated response;

KM multiple sclerosis; transplant rejection; vaccine; MHC.

XX Homo sapiens.

XX WO9404171-A1.

XX 03-MAR-1994.

XX 11-AUG-1993; 93WO-US007545.

XX 11-AUG-1992; 92US-00925460.

XX 15-JUN-1993; 93US-00077255.

XX (HARD ) HARVARD COLLEGE.

XX Urban RG, Chicz RM, Vignali DA, Hedley ML, Stern LJ;

XX Strominger JL;

XX WPI; 1994-082825/10.

XX Novel immunomodulatory peptide(s) and nucleic acids - useful for

XX treatment of autoimmune diseases, transplant rejection and for

XX vaccination.

XX Disclosure; Page 41; 139pp; English.

XX The sequences given in AAR49291-505 and AAR46981-7038 represent peptide

XX fragments of naturally-occurring immunomodulatory proteins. These

XX fragments are between 10-30 residues in length and bind to a human major

XX histocompatibility complex (MHC) class II allotype. These peptides may be

XX used for therapy of autoimmune diseases, such as type I diabetes,

XX rheumatoid arthritis and multiple sclerosis, and to reduce transplant

XX rejection. They may also be used for vaccination providing an exclusively

XX T-cell-mediated response, which can be class I or class-II based, or

XX both, depending on the length and character of the immunogenic peptides.

XX (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to

XX correct PR field.)

XX Sequence 16 AA;

XX Query Match 100.0%; Score 28; DB 2; Length 16;

XX Best Local Similarity 100.0%; Pred. No. 15;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 DYGMS 5

XX | | | | |

XX DB 3 DYGMS 7

#### RESULT 15

ABJ05002

ID ABJ05002 standard; peptide; 20 AA.  
 XX  
 AC ABJ05002;  
 XX  
 DT 30-OCT-2002 (first entry)  
 XX  
 DE A3 peptide of FVII precursor SEQ ID No 58.  
 XX  
 DE Haemostatic; antibody inhibitor; factor VIII; T cell; immune response;  
 XX haemophilia A; acquired haemophilia; human factor VIII.  
 KM  
 XX Homo sapiens.  
 OS  
 XX WO200260917-A2.  
 PN  
 XX 08-AUG-2002.  
 PD  
 XX 30-NOV-2001; 2001WO-US044945.  
 PF  
 XX 01-DEC-2000; 2000US-0250430P.  
 PR  
 XX (MINU ) UNIV MINNESOTA.  
 PA  
 XX Cont: Fine BM;  
 PI  
 XX MPI; 2002-627462/67.  
 DR  
 XX  
 XX  
 PT New peptides or their variants, useful for preventing, treating or  
 PT inhibiting aberrant or pathogenic production of antibodies specific for  
 PT factor VIII, particularly useful for treating hemophilia A or acquired  
 PT hemophilia.  
 PT  
 XX  
 PS Claim 44; Page 62; 120P; English.  
 XX  
 CC The invention relates to isolated and purified peptides and variants  
 CC thereof, as well as DNA encoding those peptides, useful to prevent or  
 CC treat antibody inhibitors of factor VIII. The peptides are useful for  
 CC preventing or inhibiting aberrant, pathogenic or undesirable antibody  
 CC production or antibody binding that is specific for factor VIII. The  
 CC peptides are also useful for preventing or inhibiting the priming or  
 CC activity of T cells specific for factor VIII. These peptides are also  
 CC useful for enhancing the activity or increasing the levels of modulatory  
 CC T cells that inhibit the immune response to factor VIII. These peptides  
 CC are useful in mammals, particularly in humans. The administration of  
 CC these peptides does not increase the synthesis of a pathogenic antibody  
 CC to factor VIII, or its biologically active fragment or functional  
 CC equivalent. In particular, these peptides are useful for treating  
 CC haemophilia A or acquired haemophilia. This sequence represents a human  
 CC factor VIII peptide region relating to the invention  
 CC  
 XX  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 28; DB 5; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYGM 5  
 |||||  
 Db 9 DYGM 13

Search completed: April 25, 2005, 20:22:28  
 Job time : 5.06541 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 20:24:31 ; Search time 0.77051 Seconds

(without alignments)  
484,413 Million cell updates/sec

Title: US-10-029-926D-114

Perfect score: 28  
Sequence: 1 DYGMS 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/1aa/5A COMB pep:.\*  
2: /cgn2\_6/prodata/1/1aa/5B COMB pep:.\*  
3: /cgn2\_6/prodata/1/1aa/6A COMB pep:.\*  
4: /cgn2\_6/prodata/1/1aa/6B COMB pep:.\*  
5: /cgn2\_6/prodata/1/1aa/PTUS COMB pep:.\*  
6: /cgn2\_6/prodata/1/1aa/backfile1 pep:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	16	2 US-08-480-190-170	Sequence 170, App
2	28	100.0	16	2 US-08-488-379-170	Sequence 170, App
3	28	100.0	16	4 US-08-475-399A-170	Sequence 170, App
4	28	100.0	16	4 US-08-077-255A-170	Sequence 170, App
5	28	100.0	16	5 PCT-US93-07545-170	Sequence 170, App
6	28	100.0	116	2 US-08-652-816A-14	Sequence 14, App
7	28	100.0	117	3 US-08-545-809A-106	Sequence 106, App
8	28	100.0	232	4 US-09-489-039A-8586	Sequence 8586, App
9	28	100.0	258	4 US-09-107-532A-4002	Sequence 4002, App
10	28	100.0	254	4 US-09-107-532A-6813	Sequence 6813, App
11	28	100.0	309	3 US-09-079-029-9	Sequence 9, App
12	28	100.0	334	3 US-08-724-984A-2	Sequence 2, App
13	28	100.0	373	4 US-09-828-995B-35	Sequence 35, App
14	28	100.0	470	4 US-09-828-995B-11	Sequence 11, App
15	28	100.0	474	4 US-09-486-192-4	Sequence 4, App
16	28	100.0	520	4 US-09-902-540-11365	Sequence 11365, App
17	28	100.0	868	1 US-07-864-004B-6	Sequence 6, App
18	28	100.0	868	1 US-08-251-937A-6	Sequence 6, App
19	28	100.0	868	1 US-08-212-133A-3	Sequence 3, App
20	28	100.0	1090	5 PCT-US93-03275-6	Sequence 6, App
21	28	100.0	1438	3 US-09-209-916-1	Sequence 1, App
22	28	100.0	1438	2 US-08-670-707A-39	Sequence 39, App
23	28	100.0	1443	3 US-09-037-601-39	Sequence 39, App
24	28	100.0	1443	3 US-09-315-179-39	Sequence 39, App
25	28	100.0	1457	4 US-09-001-039B-47	Sequence 47, App
26	28	100.0	1467	4 US-09-523-656-38	Sequence 38, App
27	28	100.0	1471	1 US-08-683-839B-3	Sequence 3, App

28	28	100.0	1661	2 US-08-882-083-2	Sequence 2, App
29	28	100.0	1661	2 US-08-558-107-2	Sequence 2, App
30	28	100.0	1661	3 US-09-243-539-2	Sequence 2, App
31	28	100.0	2115	3 US-09-324-867-5	Sequence 5, App
32	28	100.0	2133	2 US-08-670-707A-37	Sequence 37, App
33	28	100.0	2133	3 US-09-037-601-37	Sequence 37, App
34	28	100.0	2133	3 US-09-315-179-37	Sequence 37, App
35	28	100.0	2133	4 US-09-523-656-30	Sequence 30, App
36	28	100.0	2304	3 US-09-324-867-4	Sequence 4, App
37	28	100.0	2319	1 US-08-212-133A-8	Sequence 8, App
38	28	100.0	2319	1 US-08-474-503-6	Sequence 6, App
39	28	100.0	2319	2 US-08-670-707A-6	Sequence 6, App
40	28	100.0	2319	3 US-09-037-601-6	Sequence 6, App
41	28	100.0	2319	3 US-09-315-179-6	Sequence 6, App
42	28	100.0	2319	4 US-09-523-656-28	Sequence 28, App
43	28	100.0	2319	5 PCT-US94-13200-6	Sequence 6, App
44	28	100.0	2332	1 US-07-864-004B-4	Sequence 4, App
45	28	100.0	2332	1 US-08-251-937A-4	Sequence 4, App

## ALIGNMENTS

RESULT 1  
US-08-480-190-170  
; Sequence 170, Application US/08480190  
; Patent No. 5827516  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Urban  
; APPLICANT: Roman M. Chicz  
; APPLICANT: Darlo A. A. Vignali  
; APPLICANT: Mary L. Hedley  
; APPLICANT: Lawrence J. Stern  
; APPLICANT: Jack L. Strominger  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,190  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/077,255  
; FILING DATE: June 15, 1993  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: August 11, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00246/168001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 170:  
; LENGTH: 16  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-08-480-190-170

Query Match 100.0%; Score 28; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5  
|||||  
Db 3 DYGM 7

## RESULT 2

US-08-488-379-170

; Sequence 170, Application US/08488379

; Patent No. 5880103

; GENERAL INFORMATION:

; APPLICANT: Robert G. Urban

; APPLICANT: Roman M. Chiciz

; APPLICANT: Dario A. A. Vignali

; APPLICANT: Mary L. Hedley

; APPLICANT: Lawrence J. Stern

; APPLICANT: Jack L. Strominger

; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES

; NUMBER OF SEQUENCES: 274

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish &amp; Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 50z or 55sx

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: Wordperfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,379

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/077,255

; FILING DATE: June 15, 1993

; APPLICATION NUMBER: 07/925,460

; FILING DATE: August 11, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 00246/168001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 170:

; LENGTH: 16

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; US-08-488-379-170

; Query Match 100.0%; Score 28; DB 2; Length 16;

; Best Local Similarity 100.0%; Pred. No. 4.2;

; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; QY 1 DYGM 5

; |||||

; Db 3 DYGM 7

; RESULT 3

; US-08-475-399A-170

; Sequence 170, Application US/08475399A

; Patent No. 6509033

; GENERAL INFORMATION:

APPLICANT: Urban, Robert G.  
APPLICANT: Chiciz, Roman M.  
APPLICANT: Vignali, Dario A.A.  
APPLICANT: Hedley, Mary L.  
APPLICANT: Stern, Lawrence J.  
APPLICANT: Strominger, Jack L.  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 276  
CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish &amp; Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/475,399A

; FILING DATE: 07-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/077,255

; FILING DATE: 15-JUN-1993

; APPLICATION NUMBER: 07/925,460

; FILING DATE: 11-AUG-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Fraser, Janis K.

; REGISTRATION NUMBER: 34,819

; REFERENCE/DOCKET NUMBER: 00246/168003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-507

; TELEFAX: 617/542-890

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 170:

; LENGTH: 16 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; US-08-475-399A-170

; Query Match 100.0%; Score 28; DB 4; Length 16;

; Best Local Similarity 100.0%; Pred. No. 4.2;

; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; QY 1 DYGM 5

; |||||

; Db 3 DYGM 7

; RESULT 4

; US-08-077-255A-170

; Sequence 170, Application US/08077255A

; Patent No. 6696061

; GENERAL INFORMATION:

; APPLICANT: Robert G. Urban

; APPLICANT: Roman M. Chiciz

; APPLICANT: Dario A. A. Vignali

; APPLICANT: Mary L. Hedley

; APPLICANT: Lawrence J. Stern

; APPLICANT: Jack L. Strominger

; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES

; NUMBER OF SEQUENCES: 274

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish &amp; Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 50Z or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/077,255A  
FILING DATE: June 15, 1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 170:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-077-255A-170

Query Match 100.0%; Score 28; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5  
Db 3 DYGMS 7

RESULT 5  
PCT-US93-07545-170  
Sequence 170, Application PC/TUS9307545  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Scriminger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 50Z or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07545  
FILING DATE: 19930811  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 170:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
PCT-US93-07545-170

Query Match 100.0%; Score 28; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5  
Db 3 DYGMS 7

RESULT 6  
US-08-652-816A-14  
Sequence 14, Application US/08652816A  
Patent No. 5872215  
GENERAL INFORMATION:  
APPLICANT: Osbourn, JK  
APPLICANT: Allen, DJ  
APPLICANT: McCafferty, JG  
TITLE OF INVENTION: Specific binding members, materials and  
TITLE OF INVENTION: methods.  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: IBM PC compatible  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,816A  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9525004.9  
FILING DATE: 07-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-14

Query Match 100.0%; Score 28; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
Db 31 DYGMS 35

RESULT 7  
US-08-545-809A-106  
Sequence 106, Application US/08545809A  
Patent No. 6096878  
GENERAL INFORMATION:  
APPLICANT: Honjo, Tsukuru  
APPLICANT: Matsuda, Fumihiko  
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE  
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME  
NUMBER OF SEQUENCES: 145  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/545,809A  
FILING DATE: 27-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/00603  
FILING DATE: 10-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 06501/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 106:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-545-809A-106

Query Match 100.0%; Score 28; DB 3; Length 117;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
Db 50 DYGMS 54

RESULT 8  
US-09-489-039A-8586  
Sequence 8586, Application US/09489039A

Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
TITLE OF INVENTION: PREVENTION FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 8586  
LENGTH: 232  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-8586

Query Match 100.0%; Score 28; DB 4; Length 232;  
Best Local Similarity 100.0%; Pred. No. 86;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
Db 219 DYGMS 223

RESULT 9  
US-09-107-532A-4002  
Sequence 4002, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Arinello, Pamela Deneka  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781) 893-5007  
TELEFAX: (781) 893-8277  
INFORMATION FOR SEQ ID NO: 4002:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 258 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc\_feature

LOCATION: (B) LOCATION 1...258  
SEQUENCE DESCRIPTION: SEQ ID NO: 4002  
US-09-107-532A-4002

Query Match 100.0%; Score 28; DB 4; Length 258;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
DB 172 DYGMS 176

RESULT 10  
US-09-107-532A-6813  
Sequence 6813 Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneka  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 6813:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 264 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...264  
SEQUENCE DESCRIPTION: SEQ ID NO: 6813:  
US-09-107-532A-6813

Query Match 100.0%; Score 28; DB 4; Length 264;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
DB 178 DYGMS 182

RESULT 11  
US-09-079-029-9  
Sequence 9 Application US/09079029  
Patent No. 6342369  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilla W.  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuntharapai, Anan  
APPLICANT: Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9681  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-09-079-029-9

Query Match 100.0%; Score 28; DB 3; Length 309;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
DB 70 DYGMS 74

RESULT 12  
US-08-724-984A-2  
Sequence 2 Application US/08724984A  
Patent No. 6388055  
GENERAL INFORMATION:  
APPLICANT: Derk Bergema, Mary Branner, and Usman Shanon  
TITLE OF INVENTION: No. 63880551 Mouse Genomic Clone of the CC-  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road, P.O. Box 1539  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: MICROSOFT WORD  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,984A

FILING DATE: October 3, 1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: William T. Han  
REGISTRATION NUMBER: 34,344  
REFERENCE/DOCKET NUMBER: ATG50023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610 270 5024  
TELEFAX: 610 270 5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 354  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-724-984A-2

Query Match 100.0%; Score 28; DB 3; Length 354;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5  
Db 15 DYGM5 19

RESULT 13  
US-09-828-995B-35  
Sequence 35, Application US/09828995B  
Patent No. 6703360  
GENERAL INFORMATION:  
APPLICANT: Heeka Corporation  
APPLICANT: McCall, Catherine A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13  
FILE REFERENCE: AL-7  
CURRENT APPLICATION NUMBER: US/09/828,995B  
CURRENT FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 60/195,874  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: 60/195,659  
PRIOR FILING DATE: 2000-04-07  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 35  
LENGTH: 373  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-09-828-995B-35.

Query Match 100.0%; Score 28; DB 4; Length 373;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5  
Db 50 DYGM5 54

RESULT 14  
US-09-828-995B-11  
Sequence 11, Application US/09828995B  
Patent No. 6703360  
GENERAL INFORMATION:  
APPLICANT: Heeka Corporation  
APPLICANT: McCall, Catherine A.  
APPLICANT: Tang, Liang A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13  
FILE REFERENCE: AL-7  
CURRENT APPLICATION NUMBER: US/09/828,995B  
CURRENT FILING DATE: 2001-04-09

PRIOR APPLICATION NUMBER: 60/195,874  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: 60/195,659  
PRIOR FILING DATE: 2000-04-07  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 11  
LENGTH: 470  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-09-828-995B-11

Query Match 100.0%; Score 28; DB 4; Length 470;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5  
Db 50 DYGM5 54

RESULT 15  
US-09-486-192-4  
Sequence 4, Application US/09486192  
Patent No. 6521440  
GENERAL INFORMATION:  
APPLICANT: Batell, David A.  
TITLE OF INVENTION: Proteases From Gram-Positive Organisms  
FILE REFERENCE: GC386-US  
CURRENT APPLICATION NUMBER: US/09/486,192  
CURRENT FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: PCT/US98/18677  
PRIOR FILING DATE: 1998-09-08  
PRIOR APPLICATION NUMBER: EP9719637.2  
PRIOR FILING DATE: 1997-09-15  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 474  
TYPE: PRT  
ORGANISM: Schizocaccharomyces pombe  
US-09-486-192-4

Query Match 100.0%; Score 28; DB 4; Length 474;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5  
Db 349 DYGM5 353

Search completed: April 25, 2005, 21:12:13  
Job time: 0.77051 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:22:46 ; Search time 2.21175 Seconds  
(without alignments)  
752.325 Million cell updates/sec

Title: US-10-029-926d-114

Perfect score: 28  
Sequence: 1 DYGMS 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubppa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubppa/PCTUS\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep:\*
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- 12: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*
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- 18: /cgn2\_6/ptodata/2/pubppa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	5	9 US-09-832-312-73	Sequence 73, Appl
2	28	100.0	5	11 US-09-829-495-73	Sequence 73, Appl
3	28	100.0	5	15 US-10-032-037B-114	Sequence 114, App
4	28	100.0	5	15 US-10-029-988B-114	Sequence 114, App
5	28	100.0	5	15 US-10-032-423A-114	Sequence 114, App
6	28	100.0	5	15 US-10-029-926B-114	Sequence 114, App
7	28	100.0	10	16 US-10-327-598-445	Sequence 445, App
8	28	100.0	20	15 US-10-433-273-58	Sequence 58, Appl
9	28	100.0	60	15 US-10-433-273-4	Sequence 4, Appl
10	28	100.0	60	15 US-10-194-975-20	Sequence 20, Appl
11	28	100.0	98	15 US-10-308-817-60	Sequence 60, Appl
12	28	100.0	98	15 US-10-032-037B-61	Sequence 61, Appl
13	28	100.0	98	15 US-10-029-988B-61	Sequence 61, Appl

14	28	100.0	98	15	US-10-032-423A-61	Sequence 61, Appl
15	28	100.0	98	15	US-10-453-698-60	Sequence 60, Appl
16	28	100.0	98	15	US-10-029-926B-61	Sequence 61, Appl
17	28	100.0	98	16	US-10-379-392-21	Sequence 21, Appl
18	28	100.0	98	16	US-10-884-830-559	Sequence 559, App
19	28	100.0	116	16	US-10-437-963-114282	Sequence 114282, App
20	28	100.0	156	15	US-10-424-599-215325	Sequence 215325, App
21	28	100.0	239	10	US-09-880-748-937	Sequence 937, App
22	28	100.0	239	10	US-09-880-748-2015	Sequence 2015, App
23	28	100.0	239	10	US-09-880-748-2038	Sequence 2038, App
24	28	100.0	239	15	US-10-293-418-937	Sequence 937, App
25	28	100.0	239	15	US-10-293-418-2015	Sequence 2015, App
26	28	100.0	239	15	US-10-293-418-2038	Sequence 2038, App
27	28	100.0	242	17	US-10-935-290-130	Sequence 130, App
28	28	100.0	244	14	US-10-322-673-42	Sequence 42, Appl
29	28	100.0	249	17	US-10-935-290-40	Sequence 40, Appl
30	28	100.0	251	10	US-09-880-748-1542	Sequence 1542, App
31	28	100.0	251	15	US-10-293-418-1542	Sequence 1542, App
32	28	100.0	266	15	US-10-032-037B-204	Sequence 204, App
33	28	100.0	266	15	US-10-029-988B-204	Sequence 204, App
34	28	100.0	266	15	US-10-032-423A-204	Sequence 204, App
35	28	100.0	276	15	US-10-425-114-70003	Sequence 70003, A
36	28	100.0	277	15	US-10-032-037B-25	Sequence 25, Appl
37	28	100.0	277	15	US-10-032-037B-203	Sequence 203, Appl
38	28	100.0	277	15	US-10-029-988B-25	Sequence 25, Appl
39	28	100.0	277	15	US-10-029-988B-203	Sequence 203, Appl
40	28	100.0	277	15	US-10-032-423A-25	Sequence 25, Appl
41	28	100.0	277	15	US-10-032-423A-203	Sequence 203, Appl
42	28	100.0	277	15	US-10-029-926B-25	Sequence 25, Appl
43	28	100.0	277	15	US-10-029-926B-203	Sequence 203, Appl
44	28	100.0	279	15	US-10-425-114-36951	Sequence 36951, A
45	28	100.0	299	16	US-10-767-701-44522	Sequence 44522, A

#### ALIGNMENTS

RESULT 1  
US-09-832-312-73  
; Sequence 73, Application US/09832312  
; Patent No. US20010049629A1  
; GENERAL INFORMATION:  
; APPLICANT: Buefield et al.  
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF  
; FILE REFERENCE: 7853-234  
; CURRENT APPLICATION NUMBER: US/09/832,312  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/610,118  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/503,387  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: 09/454,824  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: 09/345,468  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 73  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-832-312-73

Query Match 100.0%; Score 28; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 DYGMS 5  
DB 1 DYGMS 5

RESULT 2

```
US-09-829-495-73
; Sequence 73, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villaveal J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gail DS
; APPLICANT: Olan MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-73
```

```
Query Match          100.0%; Score 28; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYGMS 5
        |||||
Db       1 DYGMS 5
```

```
RESULT 3
US-10-032-037B-114
; Sequence 114, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-114
```

```
Query Match          100.0%; Score 28; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYGMS 5
        |||||
Db       1 DYGMS 5
```

```
RESULT 4
US-10-029-988B-114
; Sequence 114, Application US/10029988B
; Publication No. US20040001839A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-114
```

```
Query Match          100.0%; Score 28; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYGMS 5
        |||||
Db       1 DYGMS 5
```

```
RESULT 5
US-10-032-423A-114
; Sequence 114, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-114
```

```
Query Match          100.0%; Score 28; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYGMS 5
        |||||
Db       1 DYGMS 5
```

```
RESULT 6
US-10-029-926B-114
; Sequence 114, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
```

ORGANISM: Homo sapiens  
US-10-029-926d-114

Query Match 100.0%; Score 28; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGS 5  
Db 1 DYGS 5

## RESULT 7

US-10-327-598-445  
Sequence 445, Application US/10327598  
Publication No. US20040181039A1  
GENERAL INFORMATION:  
APPLICANT: Krah, Eugene  
APPLICANT: Guo, Honliang  
APPLICANT: Alivappa, Ashok  
APPLICANT: Lawton, Robert  
TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and  
FILE REFERENCE: 01-799-A  
CURRENT APPLICATION NUMBER: US/10/327,598  
CURRENT FILING DATE: 2002-12-20  
PRIOR APPLICATION NUMBER: US 60/344,874  
PRIOR FILING DATE: 2001-12-21  
NUMBER OF SEQ ID NOS: 1139  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 445  
LENGTH: 10  
TYPE: PRT  
ORGANISM: canis familiaris;  
US-10-327-598-445

Query Match 100.0%; Score 28; DB 16; Length 10;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGS 5  
Db 6 DYGS 10

## RESULT 8

US-10-433-273-58  
Sequence 58, Application US/10433273  
Publication No. US20040096456A1  
GENERAL INFORMATION:  
APPLICANT: Regents of the University of Minnesota  
APPLICANT: Conti-Fine, Bianca M.  
TITLE OF INVENTION: Methods to Treat Hemophilia  
FILE REFERENCE: 600.507M01  
CURRENT APPLICATION NUMBER: US/10/433,273  
CURRENT FILING DATE: 2003-11-17  
PRIOR APPLICATION NUMBER: US 60/250,430  
PRIOR FILING DATE: 2000-12-01  
NUMBER OF SEQ ID NOS: 61  
SEQ ID NO 58  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-433-273-58

Query Match 100.0%; Score 28; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGS 5  
Db 9 DYGS 13

## RESULT 9

US-10-433-273-4  
Sequence 4, Application US/10433273  
Publication No. US20040096456A1  
GENERAL INFORMATION:  
APPLICANT: Regents of the University of Minnesota  
APPLICANT: Conti-Fine, Bianca M.  
TITLE OF INVENTION: Methods to Treat Hemophilia  
FILE REFERENCE: 600.507M01  
CURRENT APPLICATION NUMBER: US/10/433,273  
CURRENT FILING DATE: 2003-11-17  
PRIOR APPLICATION NUMBER: US 60/250,430  
PRIOR FILING DATE: 2000-12-01  
NUMBER OF SEQ ID NOS: 61  
SEQ ID NO 4  
LENGTH: 60  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-433-273-4

Query Match 100.0%; Score 28; DB 15; Length 60;  
Best Local Similarity 100.0%; Pred. No. 86;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGS 5  
Db 39 DYGS 43

## RESULT 10

US-10-194-975-20  
Sequence 20, Application US/10194975  
Publication No. US20030039649A1  
GENERAL INFORMATION:  
APPLICANT: Foote, Jefferson  
TITLE OF INVENTION: Super Humanized Antibodies  
FILE REFERENCE: 501231.01  
CURRENT APPLICATION NUMBER: US/10/194,975  
CURRENT FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: US 60/305,111  
PRIOR FILING DATE: 2001-07-12  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 20  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-194-975-20

Query Match 100.0%; Score 28; DB 14; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGS 5  
Db 31 DYGS 35

## RESULT 11

US-10-308-817-60  
Sequence 60, Application US/10308817  
Publication No. US20030219861A1  
GENERAL INFORMATION:  
APPLICANT: Roher, Russell  
APPLICANT: Wu, Dayang  
TITLE OF INVENTION: HYBRID ANTIBODIES  
FILE REFERENCE: 1087-37  
CURRENT APPLICATION NUMBER: US/10/308,817  
CURRENT FILING DATE: 2002-12-03  
NUMBER OF SEQ ID NOS: 195  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 60

LENGTH: 98  
TYPE: PRT  
ORGANISM: human  
US-10-308-817-60

Query Match 100.0%; Score 28; DB 15; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5  
Db 31 DYGM 35

RESULT 12  
US-10-032-037B-61  
Sequence 61, Application US/10032037B  
Publication No. US20040001822A1  
GENERAL INFORMATION:  
APPLICANT: Bio-Technology General Corp.  
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
TITLE OF INVENTION: MOJETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
FILE REFERENCE: 10793/44  
CURRENT APPLICATION NUMBER: US/10/032.037B  
PRIOR FILING DATE: 2001-12-31  
PRIOR APPLICATION NUMBER: 60/258,948  
PRIOR FILING DATE: 2000-12-29  
NUMBER OF SEQ ID NOS: 204  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 61  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-032-037B-61

Query Match 100.0%; Score 28; DB 15; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5  
Db 31 DYGM 35

RESULT 13  
US-10-029-988B-61  
Sequence 61, Application US/10029988B  
Publication No. US20040001839A1  
GENERAL INFORMATION:  
APPLICANT: Bio-Technology General Corp.  
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
TITLE OF INVENTION: MOJETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
FILE REFERENCE: 10793/46  
CURRENT APPLICATION NUMBER: US/10/029.988B  
CURRENT FILING DATE: 2001-12-31  
PRIOR APPLICATION NUMBER: 60/258,948  
PRIOR FILING DATE: 2000-12-29  
NUMBER OF SEQ ID NOS: 204  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 61  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-029-988B-61

Query Match 100.0%; Score 28; DB 15; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5  
Db 31 DYGM 35

RESULT 14  
US-10-032-423A-61  
Sequence 61, Application US/10032423A  
Publication No. US20040002450A1  
GENERAL INFORMATION:  
APPLICANT: Bio-Technology General Corp.  
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
TITLE OF INVENTION: MOJETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
FILE REFERENCE: 10793/45  
CURRENT APPLICATION NUMBER: US/10/032.423A  
CURRENT FILING DATE: 2001-12-31  
PRIOR APPLICATION NUMBER: 60/258,948  
PRIOR FILING DATE: 12/29/2000  
NUMBER OF SEQ ID NOS: 204  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 61  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-032-423A-61

Query Match 100.0%; Score 28; DB 15; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5  
Db 31 DYGM 35

RESULT 15  
US-10-453-698-60  
Sequence 60, Application US/10453698  
Publication No. US20040038308A1  
GENERAL INFORMATION:  
APPLICANT: Rocher, Russell  
TITLE OF INVENTION: HYBRID ANTIBODIES  
FILE REFERENCE: 82 CIP (1087-37 CIP)  
CURRENT APPLICATION NUMBER: US/10/453.698  
CURRENT FILING DATE: 2003-06-03  
NUMBER OF SEQ ID NOS: 196  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 60  
LENGTH: 98  
TYPE: PRT  
ORGANISM: human  
US-10-453-698-60

Query Match 100.0%; Score 28; DB 15; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5  
Db 31 DYGM 35

Search completed: April 25, 2005, 21:09:48  
Job time : 3.21175 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: April 25, 2005, 19:57:16 ; Search time 0.576497 Seconds  
(Without alignments)  
834.495 Million cell updates/sec

Title: US-10-029-926d-114

Perfect score: 28

Sequence: 1 DYGMS 5

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	98	2	S26928
2	28	100.0	112	2	PH1654
3	28	100.0	119	2	A43413
4	28	100.0	227	2	AB1076
5	28	100.0	268	2	H84684
6	28	100.0	268	2	T04660
7	28	100.0	334	2	H95307
8	28	100.0	340	2	H72681
9	28	100.0	411	2	S74760
10	28	100.0	448	2	AB3043
11	28	100.0	468	2	B98233
12	28	100.0	474	2	T38737
13	28	100.0	478	2	F89651
14	28	100.0	502	2	T24471
15	28	100.0	609	2	H71285
16	28	100.0	650	2	G87572
17	28	100.0	756	2	D96527
18	28	100.0	830	2	I50455
19	28	100.0	869	2	A25945
20	28	100.0	916	2	B84473
21	28	100.0	1008	2	H85055
22	28	100.0	1250	2	T27706
23	28	100.0	2133	2	T42763
24	28	100.0	2319	2	A47004
25	28	100.0	2351	1	EZHU
26	25	89.3	109	2	T47696
27	25	89.3	113	2	B36259
28	25	89.3	136	2	S35759
29	25	89.3	138	1	D69979

30	25	89.3	145	2	D69383	conserved hypochet
31	25	89.3	154	2	B61027	hypochet
32	25	89.3	171	2	S69895	helicase (BC 3.6.1
33	25	89.3	188	2	T48671	extracellular heme
34	25	89.3	203	2	T05519	hypochet
35	25	89.3	203	2	C85288	hypochet
36	25	89.3	220	2	H81048	biopolymer transpo
37	25	89.3	233	1	F69178	conserved hypochet
38	25	89.3	238	2	H70734	hypochet
39	25	89.3	250	2	C85040	hypochet
40	25	89.3	251	2	D69861	RNA polymerase sig
41	25	89.3	264	2	AF3550	phosphoglycolate p
42	25	89.3	277	2	S76396	hypochet
43	25	89.3	289	2	AI3166	hypochet
44	25	89.3	291	2	A69545	mRNA 3'-end proces
45	25	89.3	298	2	T29685	hypochet

#### ALIGNMENTS

##### RESULT 1

S26928  
Ig heavy chain V region (DP-32) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S26928  
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of  
A:Reference number: S26885; MID:93021117; PMID:1404388  
A:Accession: S26928  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-98 <TOM>  
A:Cross-references: EMBL:212334; NID:932887; PID:CAA78204.1; PID:932888  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 28; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
|||||  
Db 31 DYGMS 35

##### RESULT 2

PH1654  
Ig heavy chain V region (clone 6H9) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
C:Accession: PH1654  
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Saeseo, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyl  
A:Reference number: PH1642; MID:93301610; PMID:8315388  
A:Accession: PH1654  
A:Molecule type: mRNA  
A:Residues: 1-112 <HIL>  
A:Experimental source: B cell  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 28; DB 2; Length 112;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYGMS 5  
|||||

Db 23 DYGMS 27

## RESULT 3

A43413

Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 16-Aug-1996

C/Accession: A43413

R/Tomiyama, Y.; Brojer, E.; Rugelei, Z.M.; Shattil, S.J.; Smilneck, J.; Gorski, J.; Kum

J. Biol. Chem. 267, 18085-18097, 1992

A/Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific

A/Reference number: A43413; PMID:92388177; PMID:1517241

A/Accession: A43413

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Note: sequence extracted from NCBI backbone (NCBI:P:112815)

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/9-92/Domain: immunoglobulin homology &lt;IM&gt;

Query Match 100.0%; Score 28; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5

Db 25 DYGMS 29

## RESULT 4

AB1076

probable fimbrial chaperone protein stbB [imported] - Salmonella enterica subsp. enterica

C/Species: Salmonella enterica subsp. enterica serovar Typh

A/Note: this species has also been called Salmonella typh

C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C/Accession: AB1076

R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moutle, S.; O'Garra, P.

Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A/Reference number: AB0502; PMID:21534947; PMID:1167608

A/Accession: AB1076

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-227 &lt;PAR&gt;

A/Cross-references: GB:AL513382; PIDN:CAD03425.1; PID:G16505691; GSPDB:GN00176

C/Genetics:

A/Gene: stbB

C/Superfamily: chaperone protein papD

Query Match 100.0%; Score 28; DB 2; Length 227;

Best Local Similarity 100.0%; Pred. No. 48;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5

Db 215 DYGMS 219

## RESULT 5

H84684

En/Spm-like transposon protein [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C/Accession: H84684

R/Li, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Mofatt, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Unayam, L.; Tallon, L.;

Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: AB4420; PMID:20083487; PMID:10617197

A/Accession: H84684

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-268 &lt;STO&gt;

A/Cross-references: UNIPROT:Q9SKM6; GB:AE002093; NID:94432833; PIDN:AAD20682.1; GSPDB:G

A/Genes: AC2928440

A/Map position: 2

Query Match 100.0%; Score 28; DB 2; Length 268;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5

Db 218 DYGMS 222

## RESULT 6

T04660

hypothetical protein F8D20\_60 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004

C/Accession: T04660

R/Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mewes

submitted to the Protein Sequence Database, July 1998

A/Reference number: Z15381

A/Accession: T04660

A/Molecule type: DNA

A/Residues: 1-268 &lt;BEV&gt;

A/Cross-references: UNIPROT:O81788; EMBL:AL031135

A/Experimental source: cultivar Columbia; BAC clone F8D20

C/Genetics:

A/Map position: 4

A/Intons: 75/1; 241/1

A/Note: F8D20\_60

Query Match 100.0%; Score 28; DB 2; Length 268;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5

Db 263 DYGMS 267

## RESULT 7

H95307

arginine deiminase (EC 3.5.3.6) ArCB [imported] - Sinorhizobium meliloti (strain 1021)

C/Species: Sinorhizobium meliloti

C/Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004

C/Accession: H95307

R/Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow

A/Authors: Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A/Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo

A/Reference number: A95262; PMID:21396509; PMID:11481432

A/Accession: H95307

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-334 &lt;KUR&gt;

A/Cross-references: UNIPROT:Q922T1; GB:AE006469; PIDN:AAK65026.1; PID:G14523456; GSPDB:

A/Experimental source: strain 1021, megaplasmid pSymA

R/Galibert, F.; Finan, T.M.; Long, S.R.; Pulter, A.; Abola, P.; Ampe, F.; Barloy-Hubler

pel, D.; Chaim, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure

hebut, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K

A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A/Reference number: A96039; PMID:21368234; PMID:11474104

A:Contents: annotation  
C:Genetics:  
A:Gene: arcB  
A:Genome: plasmid  
C:Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase  
C:Keywords: hydrolase

Query Match 100.0%; Score 28; DB 2; Length 334;

Best Local Similarity 100.0%; Pred. No. 73; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5  
|||||  
DB 292 DYGM 296

## RESULT 8

H72681 hypothetical protein APE0874 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

C:Accession: H72681

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatakeyama, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum

A:Reference number: A72450; PMID:9310339; PMID:1038296

A:Accession: H72681

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-340 <KAM>

A:Cross-references: UNIPROT:Q9YDPI; DDBJ:AP000060; NID:95104188; PIDN:BA79856.1; PID:95

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE0874

C:Superfamily: Aeropyrum pernix hypothetical protein APE0874

Query Match 100.0%; Score 28; DB 2; Length 340;

Best Local Similarity 100.0%; Pred. No. 75; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5  
|||||  
DB 82 DYGM 86

## RESULT 9

S74760 hypothetical protein slr1617 - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C>Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C:Accession: S74760

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

B.

A:Reference number: S74322; PMID:97061201; PMID:8905231

A:Accession: S74760

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-411 <KAN>

A:Cross-references: UNIPROT:P72895; EMBL:D90901; GB:AB001339; NID:91651897; PIDN:BA1691

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 100.0%; Score 28; DB 2; Length 411;

Best Local Similarity 100.0%; Pred. No. 92; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5  
|||||  
DB 65 DYGM 69

## RESULT 10

AB3043 oxidoreductase Atu3958 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004

C:Accession: AB3043

R:Wood, D.W.; Seubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Moo,

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; Mclell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:21608550; PMID:11743193

A:Accession: AB3043

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-448 <KUR>

A:Cross-references: UNIPROT:Q8U8Y0; GB:AE008689; PIDN:AAU4760.1; PID:917742396; GSPDB:

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu3958

A:Map position: linear chromosome

Query Match 100.0%; Score 28; DB 2; Length 448;

Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5  
|||||  
DB 124 DYGM 128

## RESULT 11

B98243 hypothetical protein AGR\_L\_1791 [imported] - Agrobacterium tumefaciens (strain C58, Cer

C:Species: Agrobacterium tumefaciens

C>Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004

C:Accession: B98243

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman

A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu

A:Reference number: A97359; PMID:21608551; PMID:11743194

A:Accession: B98243

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-468 <KUR>

A:Cross-references: UNIPROT:Q8U8Y0; GB:AE007870; PIDN:AAK89468.1; PID:915159336; GSPDB:

A:Genetics:

A:Gene: AGR\_L\_1791

A:Map position: linear chromosome

Query Match 100.0%; Score 28; DB 2; Length 468;

Best Local Similarity 100.0%; Pred. No. 11e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5  
|||||  
DB 144 DYGM 148

## RESULT 12

T38737 probable CAAX prenyl proteinase 1 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: T38737

R:Gentles, S.; Churcher, C.M.; Bartell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, December 1995

A:Reference number: Z21808

A/Accession: T18737  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-474 <GEN>  
 A/Cross-references: UNIPROT:Q10071; EMBL:Z68144; PIDN:CAA92258.1; GSPDB:GN00066; SPDB:SF  
 A/Experimental source: strain 97zh-; cosmid c3H1  
 C/Genetics:  
 A/Gene: SPDB:SPAC3H1.05  
 A/Map position: 1  
 A/Introns: 35/3

Query Match 100.0%; Score 28; DB 2; Length 474;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
 |||||  
 Db 349 DYGMS 353

## RESULT 13

F89651  
 Protein T04F8.2 [imported] - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
 C/Accession: F89651  
 R/Anonymous, The C. elegans Sequencing Consortium.  
 Science 282, 2012-2018, 1998  
 A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
 A/Reference number: A75000; MID:99069613; PMID:9851916  
 A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C\_ele  
 A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
 A/Accession: F89651  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-478 <STO>  
 A/Cross-references: UNIPROT:Q22162; GB:chr X; PIDN:CAA91478.1; PID:G3924836; GSPDB:GN000  
 A/Note: CDNA EST EMBL:M89094 comes from this gene  
 C/Genetics:  
 A/Gene: T04F8.2  
 A/Map position: X  
 C/Superfamily: Caenorhabditis elegans hypothetical protein T04F8.2

Query Match 100.0%; Score 28; DB 2; Length 478;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
 |||||  
 Db 77 DYGMS 81

## RESULT 14

T24471  
 hypothetical protein T04F8.2 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C/Accession: T24471  
 R/Lennard, N.  
 submitted to the EMBL Data Library, November 1995  
 A/Reference number: Z19895  
 A/Accession: T24471  
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA  
 A/Residues: 1-502 <WTL>  
 A/Cross-references: UNIPROT:Q22162; EMBL:Z66565; PIDN:CAA91478.2; GSPDB:GN00028; CESP:TC  
 A/Experimental source: clone T04F8  
 C/Genetics:  
 A/Gene: CESP:T04F8.2  
 A/Map position: X  
 A/Introns: 26/1; 72/1; 103/3; 162/2; 214/3; 249/2; 290/2; 340/3; 382/2; 427/1; 459/2  
 C/Superfamily: Caenorhabditis elegans hypothetical protein T04F8.2

Query Match 100.0%; Score 28; DB 2; Length 502;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
 |||||  
 Db 93 DYGMS 97

## RESULT 15

H71285  
 Probable cell division protein (ftsH) - syphilis spirochete  
 C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
 C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
 C/Accession: H71285  
 R/Frazer, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi  
 reon, U.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; Mcb  
 they, L.; Weidman, U.; Smith, H.O.; Venter, J.C.  
 Science 281, 375-388, 1998  
 A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
 A/Reference number: A71250; MID:98332770; PMID:9665876  
 A/Accession: H71285  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-609 <COL>  
 A/Cross-references: UNIPROT:O83746; GB:AE001247; GB:AE000520; NID:G3323059; PIDN:MAC657  
 A/Experimental source: strain Nichols  
 C/Genetics:  
 A/Gene: T70765  
 C/Superfamily: cell division protein ftsH, FtsH/SEC18/CDC48-type ATP-binding domain homology <VAT>  
 F/155-363/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VAT>

Query Match 100.0%; Score 28; DB 2; Length 609;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5  
 |||||  
 Db 493 DYGMS 497

Search completed: April 25, 2005, 20:24:10  
 Job time : 2.5765 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 20:10:00 ; Search time 2.58315 seconds  
(without alignments)  
991.192 Million cell updates/sec

Title: US-10-029-926d-114  
Perfect score: 28  
Sequence: 1 DYGMS 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	70	2	Q84247
2	28	100.0	112	2	Q9HCC1
3	28	100.0	195	2	Q726K5
4	28	100.0	204	2	Q08823
5	28	100.0	204	2	Q08826
6	28	100.0	206	2	Q69K89
7	28	100.0	227	2	Q820S8
8	28	100.0	227	2	Q82J00
9	28	100.0	242	2	Q6GR19
10	28	100.0	245	2	Q6E260
11	28	100.0	246	2	Q6NU71
12	28	100.0	249	2	Q8E110
13	28	100.0	255	2	Q6GMS0
14	28	100.0	268	2	Q81788
15	28	100.0	268	2	Q9SKM6
16	28	100.0	280	2	Q742X5
17	28	100.0	293	2	Q8PFN0
18	28	100.0	300	2	Q9C840
19	28	100.0	302	2	Q9M7X8
20	28	100.0	333	2	Q6L162
21	28	100.0	334	1	Q7CC_RHME
22	28	100.0	340	2	Q9YDP1
23	28	100.0	352	2	Q6Y741
24	28	100.0	354	1	CKR5_MOUSE
25	28	100.0	361	2	Q7CCF5
26	28	100.0	362	2	Q9LTC3
27	28	100.0	406	2	Q9EYS9
28	28	100.0	411	2	P72895
29	28	100.0	439	2	Q87765
30	28	100.0	448	2	Q8U8Y0
31	28	100.0	448	2	Q880T6

32	28	100.0	468	2	Q7CTQ2	Q7ctq2 agrobacteri
33	28	100.0	474	1	ST24_SCHPO	Q10071 schizosacch
34	28	100.0	486	2	Q8L4E4	Q8l4e4 oryza sativ
35	28	100.0	493	1	OCIN_XENLA	Q9pnl1 xenopus lae
36	28	100.0	502	2	Q22162	Q22162 xenopus lae
37	28	100.0	517	2	Q6CCU2	Q6ccu2 yarrowia li
38	28	100.0	519	2	Q66J48	Q66j48 xenopus lae
39	28	100.0	532	2	Q7XR43	Q7xr43 oryza sativ
40	28	100.0	537	2	Q9LPR6	Q9lpr6 chilo iride
41	28	100.0	560	2	Q6FRU4	Q6fru4 acinetobact
42	28	100.0	572	2	P87247	P87247 botrytis ci
43	28	100.0	572	2	Q98A49	Q98a49 rhizobium i
44	28	100.0	603	2	Q899H3	Q899h3 clostridium
45	28	100.0	609	1	FTSH_TREPA	Q83746 treponema p

## ALIGNMENTS

RESULT 1	ID	Q84247	PRELIMINARY;	PRT;	70 AA.
AC	Q84247				
DT	01-JUN-2003 (Tremblrel. 24, Created)				
DT	01-JUN-2003 (Tremblrel. 24, Last sequence update)				
DT	25-OCT-2004 (Tremblrel. 28, Last annotation update)				
DE	Hypothetical protein P0458G06.105 (Hypothetical protein				
DE	OSUNBA0039C01.142).				
GN	Name=P0458G06.105; Synonyms=OSUNBA0039C01.142;				
OS	Oryza sativa (japonica cultivar-group).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OC	Erbartoideae; Oryzaceae; Oryza.				
OX	NCBI_TaxID=3947;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Sasaki T., Matsumoto T., Yamamoto K.;				
RT	"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC				
RT	clone:P0458G06."				
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Sasaki T., Matsumoto T., Katayose Y.;				
RT	"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC				
RT	clone:OSUNBA0039C01."				
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AP005051; BAC5733.1; -.				
DR	EMBL; AP005768; BAD31689.1; -.				
DR	Gramene; Q84247; -.				
KW	Hypothetical protein.				
SQ	SEQUENCE 70 AA; 7281 MW; FE752CC92EB2B855 CRC64;				
Query Match	100.0%; Score 28; DB 2; Length 70;				
Best Local Similarity	100.0%; Pred. No. 1e+02;				
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 DYGMS 5				
DB	34 DYGMS 38				
RESULT 2					
ID	Q9HCC1	PRELIMINARY;	PRT;	112 AA.	
AC	Q9HCC1				
DT	01-MAR-2001 (Tremblrel. 16, Created)				
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)				
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)				
DE	Single chain Fv (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
NCBI_TaxID=9606;					

```

RN (1)
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
DR HSSP; P01783; 1IGC.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24FLA45EC3B84788 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 112;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGSMS 5
Db 82 DYGSMS 86

RESULT 3
ID Q726K5 PRELIMINARY; PRT; 195 AA.
AC Q726K5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypochemical protein.
GN OederedocugNames=DVU3102;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OC NCBI_TaxID=882;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15077118; DOI=10.1038/nbt959;
RA Heideberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., Deboy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidson T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Uetzelback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough."
RL Nat. Biotechnol. 22:554-559(2004).
DR EMBL; AB017319; AAS97573.1; -.
DR TIGR; DVU3102; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0008565; F:protein transporter activity; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
DR InterPro; IPR006260; TonB_C.
DR TIGRfams; TIGR01352; TonB_Cterm; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 195 AA; 19904 MW; DF156A576C05C412 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 195;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGSMS 5
Db 82 DYGSMS 86

RESULT 4
ID O08823 PRELIMINARY; PRT; 204 AA.

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AC O08823;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Axonemal dynein heavy chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NR1; TISSUE=Testis;
RX MEDLINE=98038992; PubMed=9373155; DOI=10.1016/S0378-1119(97)00417-4;
RA Neesen J., Koehle M., Kirschne R., Steinlein C., Kreutzberger J.,
RA Engel W., Schmid M.;
RT "Identification of dynein heavy chain genes expressed in human and
RT mouse testis: chromosomal localization of an axonemal dynein gene."
RL Gene 200:193-202(1997).
DR EMBL; Z83810; CAB06064.1; -.
FT NON_TER 1
FT NON_TER 204
SQ SEQUENCE 204 AA; 22198 MW; 72756AAB52D0B84 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 204;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGSMS 5
Db 199 DYGSMS 203

RESULT 5
ID O08826 PRELIMINARY; PRT; 204 AA.
AC O08826;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Axonemal dynein heavy chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NR1; TISSUE=Testis;
RX MEDLINE=98038992; PubMed=9373155; DOI=10.1016/S0378-1119(97)00417-4;
RA Neesen J., Koehle M., Kirschne R., Steinlein C., Kreutzberger J.,
RA Engel W., Schmid M.;
RT "Identification of dynein heavy chain genes expressed in human and
RT mouse testis: chromosomal localization of an axonemal dynein gene."
RL Gene 200:193-202(1997).
DR EMBL; Z83813; CAB06067.1; -.
FT NON_TER 1
FT NON_TER 204
SQ SEQUENCE 204 AA; 22449 MW; 9AFDA82E4603746 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 204;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGSMS 5
Db 199 DYGSMS 203

RESULT 6
ID O69K89 PRELIMINARY; PRT; 206 AA.
AC O69K89;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

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DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)  
 DE Hypochemical protein OSUNB0079K1.23.  
 GN Name=OSUNB0079K1.23;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Erihartoideae; Oryzaceae; Oryza.  
 NCBI\_TaxID=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sasaki T., Matsumoto T., Katayose Y.;  
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, BAC  
 clone:OSUNB0079K1.1";  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AP005971; BAD36615.1; -  
 KW Hypochemical protein  
 SO SEQUENCE 206 AA; 23255 MW; 9628AC2F986F43D2 CRC64;  
 Query Match 100.0%; Score 28; DB 2; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYGMS 5  
 DB 120 DYGMS 124  
 RESULT 7  
 Q8Z0S8 PRELIMINARY; PRT; 227 AA.  
 ID Q8Z0S8  
 AC Q8Z0S8; Q7C4S5;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)  
 DE Putative fimbrial chaperone protein.  
 GN Name=ctb; OrderedLocustNames=STY4943, t4633;  
 OS Salmonella typhi.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 NCBI\_TaxID=601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;  
 RX Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,  
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagsels K.,  
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gara P., Parry C.,  
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrett B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 enterica serovar Typhi CT18";  
 RL Nature 413:848-852(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=Ty2 / ATCC 700931;  
 RX MEDLINE=22531367; PubMed=12644504;  
 RX DOI=10.1128/JB.185.7.2330-2337.2003;  
 RA Deng W., Liu S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,  
 RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;  
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2  
 and CT18";  
 RL J. Bacteriol. 185:2330-2337(2003).  
 CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the periplasmic pilus chaperone family.  
 DR EMBL: AL627284; CAP03425.1; -  
 DR EMBL: AB016849; AA072062.1; -  
 DR HSSP: P26926; 1P5U.  
 DR GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.  
 DR GO: GO:0051082; F:unfolded protein binding; IEA.  
 DR GO: GO:0007047; P:cell wall organization and biogenesis; IEA.

DR GO: GO:006457; P:protein folding; IEA.  
 DR Pfam: PF02753; Pili\_assembly\_N; 1.  
 DR Pfam: PF00345; Pili\_assembly\_C; 1.  
 DR PRINTS: PR00969; CHAPERONPili.  
 DR ProDom: PD001447; Pili\_chaperone; 1.  
 DR PROSITE: PS00635; Pili\_CHAPERONE; 1.  
 KW Chaperone; Complete proteome.  
 SO SEQUENCE 227 AA; 24829 MW; 6E8F92D7B5421AD1 CRC64;  
 Query Match 100.0%; Score 28; DB 2; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYGMS 5  
 DB 215 DYGMS 219  
 RESULT 8  
 Q8ZU0 PRELIMINARY; PRT; 227 AA.  
 ID Q8ZU0  
 AC Q8ZU0;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 26, last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)  
 DE Putative fimbrial chaperone protein.  
 GN Name=ctb; OrderedLocustNames=STM4594;  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 NCBI\_TaxID=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=LT2;  
 RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Flora L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
 LT2";  
 RL Nature 413:852-856(2001).  
 CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the periplasmic pilus chaperone family.  
 DR EMBL: AB008916; AA123409.1; -  
 DR HSSP: P26926; 1P5U.  
 DR GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.  
 DR GO: GO:0051082; F:unfolded protein binding; IEA.  
 DR GO: GO:0007047; P:cell wall organization and biogenesis; IEA.  
 DR GO: GO:006457; P:protein folding; IEA.  
 DR Pfam: PF02753; Pili\_assembly\_C; 1.  
 DR Pfam: PF00345; Pili\_assembly\_N; 1.  
 DR PRINTS: PR00969; CHAPERONPili.  
 DR ProDom: PD001447; Pili\_chaperone; 1.  
 DR PROSITE: PS00635; Pili\_CHAPERONE; 1.  
 KW Chaperone; Complete proteome.  
 SO SEQUENCE 227 AA; 24743 MW; EC0D30D9487CD7DF CRC64;  
 Query Match 100.0%; Score 28; DB 2; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYGMS 5  
 DB 215 DYGMS 219  
 RESULT 9  
 Q6GR19 PRELIMINARY; PRT; 242 AA.  
 ID Q6GR19  
 AC Q6GR19;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)

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DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE MGCG81350 protein.
GN Name=MGCG81350;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071115; AAH71115.1; -
SQ SEQUENCE 242 AA; 27476 MW; 203357C8C1AE809 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. NO. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYCGMS 5
Db 35 DYCGMS 39

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RN [1]
RP SEQUENCE FROM N.A.
RA Xiao Y., Underwood B., Moskal W., Torian U., Redman J., Wu H.C.,
RA Uterback T., Town C.D.;
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF600563; AA168362.1; -
KW Hypothetical protein.
SQ SEQUENCE 245 AA; 27802 MW; 43C5412313106AB CRC64;

Query Match 100.0%; Score 28; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. NO. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYCGMS 5
Db 40 DYCGMS 44

RESULT 11
ID 06N071; PRELIMINARY; PRT; 246 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE MGCG81187 protein.
GN Name=MGCG81187;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA MEDLINE=22368257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Klein S., Strausberg R.;
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC68729; AAH68729.1; -
DR InterPro; IPR000504; RNA_rec_mot.
PFam; PF00076; RRM_1; 1.

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DR SMART; SM00360; RRM; 1.
DR PROSITE; PSS0102; RRM; 1.
SQ SEQUENCE 246 AA; 27984 MW; 59F317B368FD6825 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 246;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5
DB 111 DYGM5 115

RESULT 12
O8E110 PRELIMINARY; PRT; 249 AA.
ID O8E110;
AC O8E110;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Prophage lambdaSal, antirepressor, putative.
DE OrderedLocNames=SAG0555;
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=2222988; PubMed=1200547; DOI=10.1073/pnas.182380799;
RA Tettein H., Maignan V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
RA Messels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radu D., Fedorova N.B., Scanlan D., Khouli H.M., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Jacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rappelli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AB014217; AAM9456.1; -.
DR TIGR; SAG0555; -.
KW Complete proteome.
SQ SEQUENCE 249 AA; 29176 MW; F6537740D2C89258 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 249;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5
DB 163 DYGM5 167

RESULT 13
O6GM50 PRELIMINARY; PRT; 255 AA.
ID O6GM50;
AC O6GM50;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE MGC83967 protein.
DE Name=MGC83967;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.T., Wang J., Heile P.,
RA Diatchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshitsuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Prange C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Klein S., Gerhard D.S.;
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC074235; AAT74235.1; -.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PR00076; RRM_1; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PSS0102; RRM; 1.
SQ SEQUENCE 255 AA; 29100 MW; 16D60836A5FD8D85 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 255;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5
DB 111 DYGM5 115

RESULT 14
O81788 PRELIMINARY; PRT; 268 AA.
ID O81788;
AC O81788;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Homodomain - like protein (AT4935550/F8D20_60) (WOX13 protein).
GN Name=F8D20_60; Synonyms=AT4935550;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Koester P., Hempel S., Entian K.-D., Hohenseil J., Jesse T.,
RA Heijnen L., Voe P., Newes H.W., Mayer K.F.X., Schueller C., Bevan M.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;

```

```

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Shin P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Banh J., Bowser L., Carninci P., Dale J.M., Gibson H.A.,
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J.,
RA Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shin P., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
RA Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.,
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Haecger A., Gross-Hardt R., Geiges B., Sarkar A., Breuninger H.,
RA Hermann M., Laux T.,
RL "expression dynamics of MOX genes mark cell fate decisions during
RT early embryonic patterning in Arabidopsis thaliana.",
RL Development 0:0-0(2004).
RN [6]
RP SEQUENCE FROM N.A.
RA Rose M., Hempel S., Ertian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.,
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AL031135; CA20025.1; -
DR EMBL; AY048268; AAK82530.1; -
DR EMBL; BT000538; AAN18107.1; -
DR EMBL; AY251404; AAP37142.1; -
DR EMBL; AL161587; CAB80271.1; -
DR PIR; T04660; T04660.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain_like.
DR Pfam; PF00046; Homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOK; 1.
DR PROSITE; PSS0071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 268 AA; 29673 MW; D57FC13AB1A93DA CRC64;

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Query Match 100.0%; Score 28; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 DYGSMS 5
Db 263 DYGSMS 267

```

```

RESULT 15
Q9SKM6 PRELIMINARY; PRT; 268 AA.
AC Q9SKM6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)

```

```

DE En/Spm-like transposon protein.
GN Name=At2g28440;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
RA Carrera A.U., Creasy T.H., Buell C.R., Town C.D., Niernan W.C.,
RA Fraser C.M., Venter J.C.,
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.,
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006283; AAD20682.1; -
DR PIR; H84684; H84684.
SQ SEQUENCE 268 AA; 27741 MW; 0584FDE4622FED0E CRC64;

```

```

Query Match 100.0%; Score 28; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DYGSMS 5
Db 218 DYGSMS 222

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Search completed: April 25, 2005, 20:34:02
Job time : 4.58315 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: April 25, 2005, 19:56:06 ; Search time 10.4224 Seconds  
(without alignments)  
630.846 Million cell updates/sec

Title: US-10-029-926D-115  
Perfect score: 96  
Sequence: 1 GINMNGSTGYADSVKX 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp19808:\*  
2: geneseqp19908:\*  
3: geneseqp20008:\*  
4: geneseqp20018:\*  
5: geneseqp20028:\*  
6: geneseqp20038:\*  
7: geneseqp20038:\*  
8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	17	AA95192	AA95192 Anti-Plat
2	96	100.0	17	ABG78240	ABG78240 Human Fv
3	96	100.0	17	ABG91931	ABG91931 Human ant
4	96	100.0	98	ABG40073	ABG40073 Anti-H1L1
5	96	100.0	98	ABG78186	ABG78186 Human Fv
6	96	100.0	98	ABG91877	ABG91877 Human ant
7	96	100.0	98	ABO27087	ABO27087 Human ger
8	96	100.0	98	ADFO9916	ADFO9916 Antibody
9	96	100.0	98	ADFI0126	ADFI0126 Antibody
10	96	100.0	98	ADFI0024	ADFI0024 VEGF anti
11	96	100.0	98	ADJ80300	ADJ80300 VH gene 1
12	96	100.0	113	AA95177	AA95177 Anti-Plat
13	96	100.0	113	AA95178	AA95178 Anti-Plat
14	96	100.0	115	AA95189	AA95189 Anti-Plat
15	96	100.0	115	AA95190	AA95190 Anti-Plat
16	96	100.0	116	AAW19880	AAW19880 CEA-speci
17	96	100.0	117	AA66312	AA66312 Human imm
18	96	100.0	118	AAU02560	AAU02560 Anti-adip
19	96	100.0	122	AA956065	AA956065 Human ant
20	96	100.0	123	ADJ57861	ADJ57861 Light var
21	96	100.0	207	AAU98019	AAU98019 Human ace
22	96	100.0	207	ADR28086	ADR28086 NFB polyp
23	96	100.0	235	AA95198	AA95198 Anti-Plat
24	96	100.0	239	ABP46004	ABP46004 Human Bly
25	96	100.0	239	ABP46027	ABP46027 Human Bly

26	96	100.0	239	5	ABP44926	ABP44926 Human Bly
27	96	100.0	239	7	ADG95753	ADG95753 Single ch
28	96	100.0	239	7	ADG96854	ADG96854 Single ch
29	96	100.0	239	7	ADG96831	ADG96831 Single ch
30	96	100.0	242	7	ADG30497	ADG30497 Human GMC
31	96	100.0	242	8	AD158068	AD158068 Reg IV-sp
32	96	100.0	244	6	AAO31136	AAO31136 Human CM0
33	96	100.0	246	5	ABG78329	ABG78329 Human Fv
34	96	100.0	246	5	ABG92026	ABG92026 Antibody
35	96	100.0	249	7	ADG30407	ADG30407 Human GMB
36	96	100.0	256	5	ABG78334	ABG78334 Human Fv
37	96	100.0	256	5	ABG92025	ABG92025 Antibody
38	96	100.0	266	5	ABG92020	ABG92020 Human ant
39	96	100.0	277	5	ABG78150	ABG78150 Human Fv
40	96	100.0	277	5	ABG78328	ABG78328 Human Fv
41	96	100.0	277	5	ABG92019	ABG92019 Human ant
42	96	100.0	277	5	ABG91841	ABG91841 Human ant
43	96	100.0	277	8	AD128366	AD128366 Human scf
44	96	100.0	278	8	AD128367	AD128367 Human scf
45	96	100.0	280	8	AD128368	AD128368 Human scf

## ALIGNMENTS

RESULT 1  
ID AA95192 standard; peptide; 17 AA.  
XX  
AC AA95192;  
XX  
DT 29-AUG-2000 (first entry)  
XX  
DE Anti-platelet glycoprotein Ib human H1b-1 VH CDR2.  
XX  
XX Variable heavy chain; single chain antibody; scFv; human; H1b-1;  
XX glycoprotein Ib alpha; platelet; aggregation; antiaggregant;  
XX antithrombotic; thrombus; therapy; diagnostic; CDR2;  
XX complementarity determining region.  
XX  
OS Homo sapiens.  
XX  
PN WO200026667-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 29-OCT-1999; 99WO-US025495.  
XX  
PR 30-OCT-1998; 98US-0106275P.  
XX  
PA (MILL.) MILLER J L.  
XX  
PI Miller JL;  
XX  
DR WPI; 2000-365744/31.  
XX  
PT Isolated nucleic acid molecule encoding anti-human platelet glycoprotein  
PT Ib alpha molecule useful for producing antibodies which inhibit platelet  
PT aggregation.  
XX  
PS Claim 15; Fig 5; 89pp; English.  
XX  
CC The present sequence is that of complementarity determining region 2  
CC (CDR2) of the heavy chain variable region (VH) of human single chain  
CC antibody (scFv) H1b-1 (see AA95198), which is directed against platelet  
CC glycoprotein Ib (GP1b). The H1b series of scFv was isolated from a human  
CC synthetic VH and VL scFv library on the basis of their binding to  
CC platelet GP1b. Whether displayed as surface proteins on a phagemid or  
CC secreted as free scFv by Escherichia coli, the H1b scFv clones are  
CC capable of inhibiting von Willebrand factor-dependent aggregation of  
CC platelets. The scFv are composed of native human protein sequences and  
CC are therefore attractive potential reagents for therapeutic purposes.  
CC They provide a new class of antithrombotic agents, useful for the

CC prevention of platelet-dependent thrombi in diseased arteries, bypass  
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.  
 CC Methods of inhibiting aggregation of platelets, of binding human platelet  
 CC GPIIb/IIIa receptor, of selecting a VH or VL region of an antibody that  
 CC inhibits platelet aggregation are claimed. Fragments of the scFv VH or VL  
 CC chain, including CDR fragments, are also claimed

XX Sequence 17 AA;

Query Match 100.0%; Score 96; DB 3; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSTGYADSVKG 17  
 1 GINWNGSTGYADSVKG 17

Db 1 GINWNGSTGYADSVKG 17

RESULT 2

ABG78240 ID ABG78240 standard; peptide; 17 AA.

XX AC ABG78240;

XX DT 15-NOV-2002 (first entry)

XX DE Human Fv molecule hypervariable region related peptide #115.

XX KM Human: Fv molecule; hypervariable region; single chain Fv; cytostatic;

XX KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukemia; adenoma;

XX KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukemia.

XX OS Homo sapiens.

XX PN WO200253700-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US049440.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

XX PI Plakain D, Peretz T;

XX DR WPI; 2002-619166/66.

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 PT or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favor of other  
 PT cells.

XX Claim 20; Page 208-209; 232p; English.

CC The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukemia cell is an  
 CC acute myeloid leukemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention

XX Sequence 17 AA;

Query Match 100.0%; Score 96; DB 5; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSTGYADSVKG 17  
 1 GINWNGSTGYADSVKG 17

Db 1 GINWNGSTGYADSVKG 17

RESULT 3

ABG91931 ID ABG91931 standard; peptide; 17 AA.

XX AC ABG91931;

XX DT 04-DEC-2002 (first entry)

XX DE Human antibody fragment #115.

XX KM Human: antibody; epitope; cancer; tumour; cell rolling; inflammation;

XX KM metastasis; hypervariable region; autoimmune disease; thrombosis;

XX KM restenosis; leukemia; inflammatory disease; cardiovascular disease;

XX KM myocardial infarction; retinopathic disease; abnormal platelet function;

XX KM sulphated tyrosine-dependent protein-protein interaction.

XX OS Homo sapiens.

XX PN WO200253700-A2.

XX PD 11-JUL-2002.

XX PF 31-DEC-2001; 2001WO-US049442.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;

XX PI Szanton E, Richter T, Amit B, Koopman L, Peretz T, Levanon A;

XX DR WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer.

XX Claim 25; Page 284-285; 0pp; English.

CC The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
 CC tumour or leukemia cells, increase in number of tumour or leukemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
 CC mortality of tumour or leukemia cells, for increasing the susceptibility  
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
 CC leukemia agents, or for decreasing the number of tumour or leukemia  
 CC cells in a patient, or in the manufacture of a medicament for the above  
 CC mentioned purposes. The epitopes are useful for diagnosing and treating  
 CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory  
 CC diseases, cardiovascular diseases such as myocardial infarction,  
 CC retinopathic diseases and other diseases mediated by abnormal platelet  
 CC function and diseases caused by sulphated tyrosine-dependent protein-  
 CC protein interactions. This sequence represents a human antibody fragment  
 CC of the invention



SQ Sequence 17 AA;  
Query Match 100.0%; Score 96; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GINWNGSGTGYADSVKG 17  
1 GINWNGSGTGYADSVKG 17  
DB 1 GINWNGSGTGYADSVKG 17

RESULT 4  
AAB40073  
ID AAB40073 standard; protein; 98 AA.  
XX AAB40073;  
AC AAB40073;  
DT 05-FEB-2001 (first entry)  
XX  
XX  
DE Anti-IL12 antibody H chain V region amino acid sequence SEQ ID 599.  
XX  
XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
KW antileukemic; neuroprotective; antipsoriatic; antiaesthetic; cardiant;  
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
KW multiple sclerosis; rheumatoid arthritis.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200056772-A1.  
PN  
XX  
XX 28-SEP-2000.  
PD  
XX  
XX 24-MAR-2000; 2000WO-US007946.  
PF  
XX  
XX 25-MAR-1999; 99US-0126603P.  
PR  
XX  
XX (BADI ) BASF AG.  
PA (BEMY ) GENETICS INST INC.  
XX  
XX Salfield JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;  
PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
PI Valdiman GM, Venturini A, Warne NW, Widom A, Bivlin JG, Duncan AR;  
PI Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL;  
XX  
XX WPI; 2000-638250/61.  
DR  
XX  
XX New human antibody specific for human interleukin-12 (IL-12) used to  
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
PT disease and multiple sclerosis.  
PS  
XX Claim 75; Page 121; 377pp; English.  
XX  
XX This invention relates to a new human antibody specific for human  
CC interleukin-12 (IL-12). The invention also includes antigen binding  
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
CC anti-IL-12 antibody heavy and light chain complementarity determining  
CC region (CDR) amino acid sequences, and also includes variable region  
CC amino acid sequences. Other variable region amino acid sequences are  
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063  
CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
CC given in AAB40064-B40067. Primers used in the identification and  
CC construction of the antibodies of the invention are given in AAC61062-  
CC C61071. The antibody of the invention is a neutralising antibody and has  
CC antirheumatic; antipsoriatic; antileukemic; antiaesthetic; cardiant;  
CC antineoplastic; antibacterial; immunosuppressive; Crohn's disease;  
CC antiparasitic; antiparasitic; antiparasitic; antiparasitic;  
CC antibacterial and immunosuppressive activity. The antibodies or antigen-  
CC binding fragments are useful in the treatment of disorders associated  
CC with detrimental release of human IL-12, especially Crohn's disease,  
CC multiple sclerosis and rheumatoid arthritis. They can also be used in the  
CC manufacture of a pharmaceutical composition to treat human IL-12  
CC disorders

XX  
SQ Sequence 98 AA;  
Query Match 100.0%; Score 96; DB 3; Length 98;  
Best Local Similarity 100.0%; Pred. No. 8.1e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GINWNGSGTGYADSVKG 17  
1 GINWNGSGTGYADSVKG 17  
DB 50 GINWNGSGTGYADSVKG 66

RESULT 5  
ABG78186  
ID ABG78186 standard; protein; 98 AA.  
XX ABG78186;  
AC ABG78186;  
DT 15-NOV-2002 (first entry)  
XX  
XX  
DE Human Fv molecule hypervariable region related peptide #61.  
XX  
XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;  
KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200259264-A2.  
PN  
XX  
XX 01-AUG-2002.  
PD  
XX  
XX 31-DEC-2001; 2001WO-US049440.  
PF  
XX  
XX 29-DEC-2000; 2000US-00751181.  
PR  
XX  
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.  
PA  
XX  
XX Hagai Y, Lazarevits J, Guy R, Lipschitz O, Szanton E, Levanon A;  
PI Plakshin D, Peretz T;  
XX  
XX WPI; 2002-619166/66.  
DR  
XX  
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
PT or fragment, or construct of fragment with enhanced binding  
PT characteristics so as to selectively bind target cell in favor of other  
PT cells.  
PS  
XX Claim 13; Page 177-178; 232pp; English.  
XX  
XX The invention relates to a peptide or polypeptide comprising an Fv  
CC molecule, a construct or fragments or a construct of a fragment with  
CC enhanced binding characteristics which selectively and/or specifically  
CC binds to a target cell in favour of other cells, where binding is  
CC primarily determined by a first hypervariable region and Fv is a single  
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
CC association with or attached, coupled, combined, linked or fused to a  
CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
CC the medicament has activity against a diseased cell, preferably a cancer  
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
CC composition for use in inhibiting the growth of a diseased or cancer  
CC cell. This sequence represents a human Fv molecule hypervariable region  
CC related peptide of the invention  
XX  
SQ Sequence 98 AA;  
Query Match 100.0%; Score 96; DB 5; Length 98;  
Best Local Similarity 100.0%; Pred. No. 8.1e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GINWNGSGTGYADSVKG 17

Db 50 GINWNGSGTGYADSVKG 66

## RESULT 6

ABG91877  
ID ABG91877 standard; protein; 98 AA.  
XX  
AC ABG91877;  
XX  
DT 04-DEC-2002 (first entry)  
XX  
DE Human antibody fragment #61.  
XX  
KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
metastasis; hypervariable region; autoimmune disease; thrombosis;  
KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
myocardial infarction; retinopathic disease; abnormal platelet function;  
KM sulphated tyrosine-dependent protein-protein interaction.  
XX  
OS Homo sapiens.  
XX  
PN WO200253700-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 31-DEC-2001; 2001WO-US049442.  
XX  
PR 29-DEC-2000; 2000US-00751181.  
PR 29-DEC-2000; 2000US-0258948P.  
XX  
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
XX  
PI Lazarevics J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
Santhanon B, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;  
WPI; 2002-674776/72.  
XX  
DR Novel isolated epitope present on cancer cells and important in  
PT physiological phenomena such as cell rolling, metastasis and  
PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
PT diseases, and cancer.  
XX  
PS Disclosure; Page 255; Ovp; English.  
XX  
CC The invention relates to an isolated epitope present on cancer cells and  
important in physiological phenomena such as cell rolling, metastasis and  
inflammation, where the epitope is capable of being bound by an antibody,  
its antigen-binding fragment or its complex comprising at least one  
antibody or its binding fragment having a first hypervariable region. The  
epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
disease, thrombosis, restenosis, metastasis, growth and/or replication of  
tumour or leukaemia cells, increase in number of tumour or leukaemia  
cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
platelet and/or cell-platelet adhesion or aggregation, for increasing  
mortality of tumour or leukaemia cells, for increasing the susceptibility  
of diseased cells to damage by anti-disease, anti-cancer or anti-  
leukaemia agents, or for decreasing the number of tumour or leukaemia  
cells in a patient, or in the manufacture of a medicament for the above  
mentioned purposes. The epitopes are useful for diagnosing and treating  
diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
diseases, cardiovascular diseases such as myocardial infarction,  
retinopathic diseases and other diseases mediated by abnormal platelet  
function and diseases caused by sulphated tyrosine-dependent protein-  
protein interactions. This sequence represents a human antibody fragment  
of the invention  
CC  
XX  
SQ Sequence 98 AA;

Query Match 100.0%; Score 96; DB 5; Length 98;  
Best Local Similarity 100.0%; Pred. No. 8.1e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVKG 17  
Db 50 GINWNGSGTGYADSVKG 66

## RESULT 7

ABO27087  
ID ABO27087 standard; protein; 98 AA.  
XX  
AC ABO27087;  
XX  
DT 10-SEP-2003 (first entry)  
XX  
DE Human germline heavy chain variable region gene segment #20.  
XX  
KW Human; heavy chain variable region; VH; humanised antibody;  
chimeric antibody; complementarity determining region; CDR;  
KM canonical CDR structure type.  
XX  
OS Homo sapiens.  
XX  
PN US2003039649-A1.  
XX  
PD 27-FEB-2003.  
XX  
PF 12-JUL-2002; 2002US-00194975.  
XX  
PR 12-JUL-2001; 2001US-0305111P.  
XX  
PA (FOOTE) FOOTE J.  
XX  
PI Foote J;  
XX  
DR WPI; 2003-492151/46.  
XX  
PT Making humanized antibody for converting antibody, by making chimeric  
PT antibodies containing complementarity determining region from non-human  
PT antibody and appropriate framework sequences of human antibodies.  
XX  
PS Example 1; Fig 1; 31pp; English.  
XX  
CC The invention describes a method of making a humanised antibody,  
comprising making chimeric antibodies containing a complementarity  
CC determining region (CDR) from a non-human antibody and appropriate  
CC framework sequences (I) of human antibodies. (I) is selected by using  
CC canonical CDR structure types of non-human antibody in comparison to  
CC germline canonical CDR structure types of human antibodies as the basis  
for selection, for humanisation. The method is useful for making a  
CC humanised antibody or a converted antibody. The method is applicable for  
CC converting a subject antibody sequence of any subject species to a less  
CC immunogenic form suitable for use in an object species. The method is  
CC reliable for identifying suitable human framework sequences to support  
CC non-human CDR regions and to provide humanised antibodies that retain  
CC high antigen binding with low immunogenicity in humans, without the need  
CC for direct comparison of framework sequences, without the need for  
CC determining critically important amino acid residues in the framework,  
CC and without the need for multiple iteration and construction to obtain  
CC humanised antibodies with suitable therapeutic properties. The antibody  
CC has high affinity and low immunogenicity without need for comparing  
CC framework sequences between non-human and human antibodies. This sequence  
CC represents a human heavy chain variable region gene segment used in the  
creation of humanised antibodies  
CC  
XX  
SQ Sequence 98 AA;

Query Match 100.0%; Score 96; DB 6; Length 98;  
Best Local Similarity 100.0%; Pred. No. 8.1e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVKG 17  
Db 50 GINWNGSGTGYADSVKG 66

```
RESULT 8
ID ADF09916 standard; protein; 98 AA.
XX
XX ADF09916;
XX
XX 12-FEB-2004 (first entry)
XX
DE Antibody heavy chain variable region VH_3-20.
XX
XX Antibody; stability; solubility; antigen binding affinity;
XX variable region; human.
XX
XX Homo sapiens.
XX
XX WO2003074679-A2.
XX
XX 12-SEP-2003.
XX
XX 03-MAR-2003; 2003WO-US006598.
XX
XX 01-MAR-2002; 2002US-0360843P.
XX
XX 29-MAY-2002; 2002US-0384197P.
XX
XX (XENC-) XENCOR.
XX
XX Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
XX WPI; 2003-722066/68.
XX
XX Computer optimization of physicochemical properties of antibodies
XX comprises analyzing the interactions of amino acids at variable
XX positions.
XX
XX Disclosure; Fig 2a; 135pp; English.
XX
XX The present invention relates to a method for optimizing at least one
XX physico-chemical property of an antibody by a computational screening
XX method. The method comprises: receiving a template antibody structure;
XX selecting at least one variable position belonging to the antibody
XX structure; selecting at least one amino acid to be considered at the
XX variable position(s); analyzing the interaction of each selected amino
XX acid at each variable position with at least part of the remainder of the
XX antibody, including the selected amino acids at other variable positions;
XX and identifying a set of at least one antibody sequence with at least one
XX optimized physico-chemical property. The method is useful for optimizing
XX the physico-chemical properties of an antibody, especially the stability,
XX solubility, or antigen binding affinity. The optimized antibody may be
XX useful for treating a patient. The present sequence is an antibody
XX variable region sequence used to illustrate the invention.
XX
SQ Sequence 98 AA;
XX
Query Match 100.0%; Score 96; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GINWNGSGTGYADSVKG 17
DB 50 GINWNGSGTGYADSVKG 66
XX
RESULT 9
ID ADF10126 standard; protein; 98 AA.
XX
XX ADF10126;
XX
XX 12-FEB-2004 (first entry)
XX
XX Antibody heavy chain variable region VH_3-20.
XX
XX
```

```
KW Antibody; stability; solubility; antigen binding affinity;
XX variable region; human.
XX
XX Homo sapiens.
XX
XX WO2003074679-A2.
XX
XX 12-SEP-2003.
XX
XX 03-MAR-2003; 2003WO-US006598.
XX
XX 01-MAR-2002; 2002US-0360843P.
XX
XX 29-MAY-2002; 2002US-0384197P.
XX
XX (XENC-) XENCOR.
XX
XX Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
XX WPI; 2003-722066/68.
XX
XX Computer optimization of physicochemical properties of antibodies
XX comprises analyzing the interactions of amino acids at variable
XX positions.
XX
XX Example 16; Fig 40a; 135pp; English.
XX
XX The present invention relates to a method for optimizing at least one
XX physico-chemical property of an antibody by a computational screening
XX method. The method comprises: receiving a template antibody structure;
XX selecting at least one variable position belonging to the antibody
XX structure; selecting at least one amino acid to be considered at the
XX variable position(s); analyzing the interaction of each selected amino
XX acid at each variable position with at least part of the remainder of the
XX antibody, including the selected amino acids at other variable positions;
XX and identifying a set of at least one antibody sequence with at least one
XX optimized physico-chemical property. The method is useful for optimizing
XX the physico-chemical properties of an antibody, especially the stability,
XX solubility, or antigen binding affinity. The optimized antibody may be
XX useful for treating a patient. The present sequence is an antibody
XX variable region sequence used to illustrate the invention.
XX
SQ Sequence 98 AA;
XX
Query Match 100.0%; Score 96; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GINWNGSGTGYADSVKG 17
DB 50 GINWNGSGTGYADSVKG 66
XX
RESULT 10
ID ADF10024 standard; protein; 98 AA.
XX
XX ADF10024;
XX
XX 12-FEB-2004 (first entry)
XX
XX VEGF antibody heavy chain variable region VH_3-20.
XX
XX Antibody; stability; solubility; antigen binding affinity;
XX variable region; human; VEGF.
XX
XX Homo sapiens.
XX
XX WO2003074679-A2.
XX
XX 12-SEP-2003.
XX
XX 03-MAR-2003; 2003WO-US006598.
XX
```

PR 01-MAR-2002; 2002US-0360843P.  
 PR 29-MAY-2002; 2002US-0384197P.  
 XX (XENC-) XENCOR.  
 XX PA  
 XX PI Lazar GA, Desjarlais JR, Marshall SA, Dahiya B,  
 DR WPI; 2003-722066/68.  
 XX  
 PT Computer optimization of physicochemical properties of antibodies  
 PT comprises analyzing the interactions of amino acids at variable  
 PT positions.  
 XX  
 PS Example 6; Fig 16a; 135pp; English.  
 CC The present invention relates to a method for optimizing at least one  
 CC physico-chemical property of an antibody by a computational screening  
 CC method. The method comprises: receiving a template antibody structure;  
 CC selecting at least one variable position belonging to the antibody  
 CC structure; selecting at least one amino acid to be considered at the  
 CC variable position(s); analyzing the interaction of each selected amino  
 CC acid at each variable position with at least part of the remainder of the  
 CC antibody, including the selected amino acids at other variable positions;  
 CC and identifying a set of at least one antibody sequence with at least one  
 CC optimized physico-chemical property. The method is useful for optimizing  
 CC the physico-chemical properties of an antibody, especially the stability,  
 CC solubility, or antigen binding affinity. The optimized antibody may be  
 CC useful for treating a patient. The present sequence is an antibody  
 CC variable region sequence used to illustrate the invention.  
 SQ Sequence 98 AA;

Query Match 100.0%; Score 96; DB 7; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GINWNGSGTGYADSVKG 17  
 Db 50 GINWNGSGTGYADSVKG 66

RESULT 11  
 ADJ80300  
 ID ADJ80300 standard; protein; 98 AA.  
 XX  
 AC ADJ80300;  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE VH gene locus antibody amino acid sequence #20.  
 XX  
 KM hybrid antibody; antibody; framework region; immunogenicity.  
 OS Homo sapiens.  
 XX  
 PN WO2003048321-A2.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 03-DEC-2002; 2002WO-US038450.  
 XX  
 PR 03-DEC-2001; 2001US-0336591P.  
 XX  
 PA (ALEX-) ALEXION PHARM INC.  
 XX  
 PI Rother R, Wu D;  
 DR WPI; 2003-513753/48.  
 XX  
 PT Producing a hybrid antibody or hybrid antibody fragment by operatively  
 PT linking the selected framework sequences to one or more complementarily  
 PT determining regions of the initial antibody.  
 XX

PS Disclosure; SEQ ID NO 60; 77pp; English.  
 XX  
 XX The invention relates to a method of producing a hybrid antibody or  
 CC hybrid antibody fragment by: (i) providing an initial antibody having  
 CC specificity for a target; (ii) determining the sequence of a variable  
 CC region of the initial antibody; (iii) selecting a first component of the  
 CC variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the  
 CC sequence of the first component to sequences contained in a reference  
 CC database of antibody sequences or antibody fragment sequences from a  
 CC target species; (v) selecting a sequence from an antibody in the database  
 CC which demonstrates a high degree of homology to the first component; (vi)  
 CC selecting a second component of the variable region which is different  
 CC than the first component; the second component selected from the group  
 CC consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the  
 CC second component to sequences contained in a reference database of  
 CC antibody sequences or antibody fragment sequences from the target species  
 CC; (viii) selecting a sequence from the database which demonstrates a high  
 CC degree of homology to the second component and which is from a different  
 CC antibody than the selected antibody; and (ix) operatively linking the  
 CC selected framework sequences to one or more complementarily determining  
 CC regions (CDRs) of the initial antibody to produce a hybrid antibody or  
 CC hybrid antibody fragment. The method is useful for producing a hybrid  
 CC antibody or hybrid antibody fragment (claimed). The antibody and  
 CC fragments are useful for therapeutic and diagnostic purposes. The method  
 CC uses entire framework regions from a single antibody variable heavy or  
 CC variable light chain to receive the CDRs. This produces antibodies that  
 CC are highly homologous and exhibit reduced immunogenicity while  
 CC maintaining an optimum binding profile. This sequence represents the  
 CC amino acid sequence of an antibody from the VH gene locus.  
 SQ Sequence 98 AA;

Query Match 100.0%; Score 96; DB 7; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GINWNGSGTGYADSVKG 17  
 Db 50 GINWNGSGTGYADSVKG 66

RESULT 12  
 AAY95177  
 ID AAY95177 standard; protein; 113 AA.  
 XX  
 AC AAY95177;  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE Anti-platelet glycoprotein Ib human H1b-1 VH.  
 XX  
 KM Variable heavy chain; single chain antibody; scFv; human; H1b-1;  
 KM glycoprotein Ib alpha; platelet; aggregation; antiaggregant;  
 KM antithrombotic; thrombus; therapy; diagnostic.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 XX  
 FT Region Location/Qualifiers  
 FT Region 1.30  
 FT Region /note="framework region 1"  
 FT Region 31..34  
 FT Region /note="complementarily determining region 1"  
 FT Region 35..49  
 FT Region /note="framework region 2"  
 FT Region 50..66  
 FT Region /note="complementarily determining region 2"  
 FT Region 67..98  
 FT Region /note="framework region 3"  
 FT Region 99..104  
 FT Region /note="complementarily determining region 3"  
 FT Region 105..113  
 FT Region /note="framework region 4"  
 XX

PN WO200026667-A1.  
 XX 11-MAY-2000.  
 XX 29-OCT-1999; 99WO-US025495.  
 XX 30-OCT-1998; 98US-0106275P.  
 XX (MILLER) MILLER J L.  
 PA Miller JL;  
 PI MPI; 2000-365744/31.  
 DR N-PSDB; AAA27658.  
 XX  
 PT Isolated nucleic acid molecule encoding anti-human platelet glycoprotein  
 PT id alpha molecule useful for producing antibodies which inhibit platelet  
 PT aggregation.  
 XX  
 PS Claim 10; Page 71; 89pp; English.  
 XX  
 CC The present sequence is that of the heavy chain variable region (VH) of  
 CC human single chain antibody (scFv) Hib-1 (see AAY95178), which is  
 CC directed against platelet glycoprotein Ib (GPIb). The Hib series of scFv  
 CC is isolated from a human synthetic VH and VL scFv library by 3 rounds of  
 CC phagemid selection against transfected CHO cells expressing the GPIb  
 CC alpha component of the GPIb/IX/V complex on their surface, followed by a  
 CC 4th round of selection against washed human platelets, and 2 final rounds  
 CC in which attempts were made to displace scFv from washed platelets by  
 CC flooding with murine monoclonal antibody or mimotope peptide (see  
 CC AAY95229). Whether displayed as surface proteins on a phagemid or  
 CC secreted as free scFv by Escherichia coli, the Hib scFv clones are  
 CC capable of inhibiting von Willebrand factor-dependent aggregation of  
 CC platelets. The scFv are composed of native human protein sequences and  
 CC are therefore attractive potential reagents for therapeutic purposes.  
 CC They provide a new class of antithrombotic agents, useful for the  
 CC prevention of platelet-dependent thrombi in diseased arteries, bypass  
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.  
 CC Methods of inhibiting aggregation of platelets, of binding human platelet  
 CC GPIb alpha and of selecting a VH or VL region of an antibody that  
 CC inhibits platelet aggregation are claimed  
 XX  
 SO Sequence 113 AA;  
 Query Match 100.0%; Score 96; DB 3; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GINWNGSTGYADSVKG 17  
 Db 50 GINWNGSTGYADSVKG 66  
 RESULT 13  
 ID AAY95178 standard; protein; 113 AA.  
 XX  
 AC AAY95178;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE Anti-platelet glycoprotein Ib human Hib-1 VH.  
 XX  
 KW Variable heavy chain; single chain antibody; scFv; human; Hib-1;  
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;  
 KW antithrombotic; thrombus; therapy; diagnostic.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Location/Qualifiers  
 FT Region 1..30  
 FT /note= "framework region 1"  
 FT Region 31..34

FT /note= "complementarity determining region 1"  
 FT Region 35..49  
 FT /note= "framework region 2"  
 FT Region 50..66  
 FT /note= "complementarity determining region 2"  
 FT Region 67..98  
 FT /note= "framework region 3"  
 FT Region 99..104  
 FT /note= "complementarity determining region 3"  
 FT Region 105..113  
 FT /note= "framework region 4"  
 PN WO200026667-A1.  
 XX 11-MAY-2000.  
 XX 29-OCT-1999; 99WO-US025495.  
 XX 30-OCT-1998; 98US-0106275P.  
 XX (MILLER) MILLER J L.  
 PA Miller JL;  
 PI MPI; 2000-365744/31.  
 DR  
 XX  
 PT Isolated nucleic acid molecule encoding anti-human platelet glycoprotein  
 PT id alpha molecule useful for producing antibodies which inhibit platelet  
 PT aggregation.  
 XX  
 PS Claim 10; Page; 89pp; English.  
 XX  
 CC The present sequence is that of the heavy chain variable region (VH) of  
 CC human single chain antibody (scFv) Hib-1 (see AAY95198), which is  
 CC directed against platelet glycoprotein Ib (GPIb). The Hib series of scFv  
 CC was isolated from a human synthetic VH and VL scFv library by 3 rounds of  
 CC phagemid selection against transfected CHO cells expressing the GPIb  
 CC alpha component of the GPIb/IX/V complex on their surface, followed by a  
 CC 4th round of selection against washed human platelets, and 2 final rounds  
 CC in which attempts were made to displace scFv from washed platelets by  
 CC flooding with murine monoclonal antibody or mimotope peptide (see  
 CC AAY95229). Whether displayed as surface proteins on a phagemid or  
 CC secreted as free scFv by Escherichia coli, the Hib scFv clones are  
 CC capable of inhibiting von Willebrand factor-dependent aggregation of  
 CC platelets. The scFv are composed of native human protein sequences and  
 CC are therefore attractive potential reagents for therapeutic purposes.  
 CC They provide a new class of antithrombotic agents, useful for the  
 CC prevention of platelet-dependent thrombi in diseased arteries, bypass  
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.  
 CC Methods of inhibiting aggregation of platelets, of binding human platelet  
 CC GPIb alpha and of selecting a VH or VL region of an antibody that  
 CC inhibits platelet aggregation are claimed. Note: The present sequence is  
 CC not shown in the specification but is derived from the Hib-1 VH sequence  
 CC given on page 71 (see AAY95177)  
 XX  
 SO Sequence 113 AA;  
 Query Match 100.0%; Score 96; DB 3; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GINWNGSTGYADSVKG 17  
 Db 50 GINWNGSTGYADSVKG 66  
 RESULT 14  
 ID AAY95189 standard; protein; 115 AA.  
 XX  
 AC AAY95189;  
 XX  
 DT 29-AUG-2000 (first entry)

XX	DE	Anti-platelet glycoprotein Ib human Hib-1 VH.	
XX	KW	Variable heavy chain; single chain antibody; scFv; human, Hib-1;	
KW	KM	glycoprotein Ib alpha; platelet; aggregation; antiaggregant;	
KM	KX	antithrombotic; thrombus; therapy; diagnostic.	
OS	XX	Homo sapiens.	
XX	FT	Key	Location/Qualifiers
FT	FT	Region	1..30
FT	FT	Region	/note= "framework region 1"
FT	FT	Region	31..34
FT	FT	Region	/note= "complementarily determining region 1"
FT	FT	Region	35..49
FT	FT	Region	/note= "framework region 2"
FT	FT	Region	50..66
FT	FT	Region	/note= "complementarily determining region 2"
FT	FT	Region	67..98
FT	FT	Region	/note= "framework region 3"
FT	FT	Region	99..104
FT	FT	Region	/note= "complementarily determining region 3"
FT	FT	Region	105..115
FT	FT	Region	/note= "framework region 4"
XX	PN	WO200026667-A1.	
XX	PD	11-MAY-2000.	
XX	PF	29-OCT-1999;	99WO-US025495.
XX	PR	30-OCT-1998;	98US-0106275P.
XX	PA	(MILLER) MILLER J L.	
XX	PI	Miller JL;	
XX	DR	WPI; 2000-365744/31.	
XX	PT	Isolated nucleic acid molecule encoding anti-human platelet glycoprotein	
XX	PT	Ib alpha molecule useful for producing antibodies which inhibit platelet	
XX	PT	aggregation.	
XX	PS	Claim 13; Fig 5; 89pp; English.	
XX	CC	The present sequence is that of the heavy chain variable region (VH) of	
XX	CC	human single chain antibody (scFv) Hib-1 (see AAY95198), which is	
XX	CC	directed against platelet glycoprotein Ib (GPiB). The Hib series of scFv	
XX	CC	was isolated from a human synthetic VH and VL scFv library by 3 rounds of	
XX	CC	phagemid selection against transfected CHO cells expressing the GPiB	
XX	CC	alpha component of the GPiB/IX/V complex on their surface, followed by a	
XX	CC	4th round of selection against washed human platelets, and 2 final rounds	
XX	CC	in which attempts were made to displace scFv from washed platelets by	
XX	CC	flooding with murine monoclonal antibody or minotope peptide (see	
XX	CC	AAY95229). Whether displayed as surface proteins on a phagemid or	
XX	CC	secreted as free scFv by Escherichia coli, the Hib scFv clones are	
XX	CC	capable of inhibiting von Willebrand factor-dependent aggregation of	
XX	CC	platelets. The scFv are composed of native human protein sequences and	
XX	CC	are therefore attractive potential reagents for therapeutic purposes.	
XX	CC	They provide a new class of antithrombotic agents, useful for the	
XX	CC	prevention of platelet-dependent thrombi in diseased arteries, bypass	
XX	CC	grafts, dialysis etc., and can also be used as diagnostic reagents.	
XX	CC	Methods of inhibiting aggregation of platelets, of binding human platelet	
XX	CC	GPiB alpha and of selecting a VH or VL region of an antibody that	
XX	CC	inhibits platelet aggregation are claimed	
XX	SQ	Sequence 115 AA;	
XX	XX	Query Match	100.0%; Score 96; DB 3; Length 115;
XX	XX	Best Local Similarity	100.0%; Pred. No. 9,7e-07;
XX	XX	Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX	XX	1 GINWNGSGTGADSVKG 17	

[illegible]

CC Methods of inhibiting aggregation of platelets, of binding human platelet  
 CC GPIIb alpha and of selecting a VH or VL region of an antibody that  
 CC inhibits platelet aggregation are claimed. Note: The present sequence is  
 CC not shown in the specification but is derived from the H1b-1 VH sequence  
 CC given in Fig 5 (see AA195189)  
 XX  
 SQ Sequence 115 AA;

Query Match 100.0%; Score 96; DB 3; Length 115;  
 Best Local Similarity 100.0%; Pred. No. 9.7e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGYADSVKG 17  
 |||||  
 Db 50 GINWNGSGTGYADSVKG 66

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OM protein - protein search, using sw model

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(without alignments)  
484,413 Million cell updates/sec

Title: US-10-029-926d-115

Perfect score: 96

Sequence: 1 GINMNGSTGYADSVKVG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	116	2	US-08-652-816A-14
2	96	100.0	117	3	US-08-545-809A-106
3	96	100.0	309	3	US-09-079-029-9
4	79	82.3	17	4	US-09-424-840B-109
5	79	82.3	118	3	US-08-545-809A-97
6	79	82.3	119	4	US-09-840-459-88
7	79	82.3	119	4	US-09-497-625A-88
8	79	82.3	120	2	US-08-958-201-8
9	79	82.3	120	2	US-08-958-201-10
10	74	74.0	149	4	US-08-471-276-898
11	74	74.0	17	4	US-08-424-840B-114
12	71	74.0	117	3	US-08-545-809A-119
13	71	74.0	118	3	US-08-545-809A-125
14	71	74.0	124	4	US-09-424-840B-18
15	68	70.8	117	1	US-07-942-245-24
16	68	70.8	126	4	US-09-232-290-35
17	66	68.8	17	4	US-09-424-840B-70
18	66	68.8	17	4	US-09-424-840B-78
19	66	68.8	124	4	US-09-424-840B-123
20	63	65.6	126	3	US-08-983-607-86
21	62.5	65.1	117	3	US-09-157-370-1
22	62	64.6	17	1	US-08-264-093-22
23	62	64.6	89	4	US-09-840-459-48
24	62	64.6	89	4	US-09-497-625A-48
25	62	64.6	111	4	US-09-899-896-7
26	62	64.6	118	2	US-08-652-816A-11
27	62	64.6	120	1	US-08-264-093-14

28	62	64.6	268	4	US-09-976-118-1	Sequence 1, Appl
29	62	64.6	483	3	US-09-049-672A-5	Sequence 5, Appl
30	61.5	64.1	95	3	US-09-043-514-2	Sequence 2, Appl
31	61.5	64.1	116	3	US-08-545-809A-135	Sequence 135, App
32	61	63.5	113	3	US-08-974-899-6	Sequence 6, Appl
33	61	63.5	113	4	US-09-795-798-6	Sequence 6, Appl
34	61	63.5	116	3	US-09-184-658-48	Sequence 48, Appl
35	61	63.5	116	3	US-08-983-607-36	Sequence 36, Appl
36	61	63.5	116	4	US-09-504-262D-48	Sequence 80, Appl
37	61	63.5	116	4	US-09-840-459-80	Sequence 80, Appl
38	61	63.5	116	4	US-09-497-625A-80	Sequence 80, Appl
39	61	63.5	117	3	US-08-545-809A-103	Sequence 103, App
40	61	63.5	117	3	US-08-545-809A-109	Sequence 109, App
41	61	63.5	117	3	US-08-983-607-46	Sequence 46, Appl
42	61	63.5	117	4	US-09-840-459-83	Sequence 83, Appl
43	61	63.5	117	4	US-09-497-625A-83	Sequence 83, Appl
44	61	63.5	118	2	US-08-652-816A-12	Sequence 12, Appl
45	61	63.5	119	4	US-09-648-067A-15	Sequence 15, Appl

## ALIGNMENTS

RESULT 1  
US-08-652-816A-14  
; Sequence 14, Application US/08652816A  
; Patent No. 5872215  
; GENERAL INFORMATION:  
; APPLICANT: Osborn, JK  
; APPLICANT: Allen, DJ  
; TITLE OF INVENTION: Specific binding members, materials and  
; TITLE OF INVENTION: methods.  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; City: Chicago  
; State: Illinois  
; COUNTRY: United States of America  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Releasee #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,816A  
; FILING DATE: 23-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9125579.4  
; FILING DATE: 02-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9125579.8  
; FILING DATE: 02-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206372.6  
; FILING DATE: 23-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9525004.9  
; FILING DATE: 07-DEC-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9610824.6  
; FILING DATE: 23-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/02240  
; FILING DATE: 02-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/244,597  
; FILING DATE: 01-JUN-1994  
; ATTORNEY/AGENT INFORMATION:

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; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 17
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-424-840B-109

Query Match      82.3%; Score 79; DB 4; Length 17;
Best Local Similarity 82.4%; Pred. No. 8.3e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1 GINWNGSTGYADSVKG 17
Db      1 GISMNGSISGYADSVKG 17

RESULT 5
US-08-545-809A-97
; Sequence 97, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsumura, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-97

Query Match      82.3%; Score 79; DB 3; Length 118;
Best Local Similarity 82.4%; Pred. No. 0.00061;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1 GINWNGSTGYADSVKG 17
Db      69 GISMNGSISGYADSVKG 85

RESULT 6
US-09-840-459-88
; Sequence 88, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
```

```
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-88

Query Match      82.3%; Score 79; DB 4; Length 119;
Best Local Similarity 82.4%; Pred. No. 0.00061;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1 GINWNGSTGYADSVKG 17
Db      50 GISMNGSISGYADSVKG 66

RESULT 7
US-09-497-625A-88
; Sequence 88, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-497-625A-88

Query Match      82.3%; Score 79; DB 4; Length 119;
Best Local Similarity 82.4%; Pred. No. 0.00061;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1 GINWNGSTGYADSVKG 17
Db      50 GISMNGSISGYADSVKG 66

RESULT 8
US-08-958-201-8
; Sequence 8, Application US/08958201
```

Patent No. 5977319  
GENERAL INFORMATION:  
APPLICANT: Pope, Anthony R  
APPLICANT: Pritchard, Kevin  
APPLICANT: Williams, Andrew J  
APPLICANT: Johnson, Kevin S  
TITLE OF INVENTION: Specific binding members for estradiol;  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/958,201  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/028,897  
FILING DATE: 21-OCT-1996  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: 2D  
US-08-958-201-8

Query Match 82.3%; Score 79; DB 2; Length 120;  
Best Local Similarity 82.4%; Pred. No. 0.00062;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSTGYADSVKG 17  
||:|||||  
Db 50 GISWNGSIGYADSVKG 66

RESULT 9  
US-08-958-201-10  
Sequence 10, Application US/08958201  
Patent No. 5977319  
GENERAL INFORMATION:  
APPLICANT: Pope, Anthony R  
APPLICANT: Pritchard, Kevin  
APPLICANT: Williams, Andrew J  
APPLICANT: Johnson, Kevin S  
TITLE OF INVENTION: Specific binding members for estradiol;  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/958,201  
FILING DATE:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/028,897  
FILING DATE: 21-OCT-1996  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: 2Db  
US-08-958-201-10

Query Match 82.3%; Score 79; DB 2; Length 120;  
Best Local Similarity 82.4%; Pred. No. 0.00062;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSTGYADSVKG 17  
||:|||||  
Db 50 GISWNGSIGYADSVKG 66

RESULT 10  
US-09-471-276-898  
Sequence 898, Application US/09471276  
Patent No. 6822072  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: GENSET.025CPI  
CURRENT APPLICATION NUMBER: US/09/471,276  
CURRENT FILING DATE: 1999-12-21  
EARLIER APPLICATION NUMBER: 09/057,719  
EARLIER FILING DATE: 1998-04-09  
EARLIER APPLICATION NUMBER: 09/069,047  
EARLIER FILING DATE: 1998-04-28  
EARLIER APPLICATION NUMBER: PCT/IB99/00712  
EARLIER FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 1622  
SOFTWARE: Patent.pm  
SEQ ID NO 898  
LENGTH: 149  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -19..-1  
US-09-471-276-898

Query Match 77.1%; Score 74; DB 4; Length 149;  
Best Local Similarity 76.5%; Pred. No. 0.0039;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GINWNGSTGYADSVKG 17  
||:|||||  
Db 69 GITWNGXIGYADSVKG 85

RESULT 11  
US-09-424-840B-114  
Sequence 114, Application US/09424840B  
Patent No. 679038  
GENERAL INFORMATION:  
APPLICANT: Berchold, Peter  
APPLICANT: Escher, Robert F. A.  
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES  
FILE REFERENCE: 100564-09049  
CURRENT APPLICATION NUMBER: US/09/424,840B  
CURRENT FILING DATE: 1999-12-03  
PRIOR APPLICATION NUMBER: DE 19820663.1  
PRIOR FILING DATE: 1998-05-08  
PRIOR APPLICATION NUMBER: DE 19755227.7

;; PRIOR FILING DATE: 1997-12-12  
;; PRIOR APPLICATION NUMBER: DE 19723904.8  
;; PRIOR FILING DATE: 1997-06-06  
;; NUMBER OF SEQ ID NOS: 128  
;; SOFTWARE: Patentin version 3.1  
;; SEQ ID NO 114  
;; LENGTH: 17  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-424-840B-114

Query Match 74.0%; Score 71; DB 4; Length 17;  
Best Local Similarity 70.6%; Pred. No. 0.0011;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINMGSTGYADSVKG 17  
DB 1 GISWDSGTIGYADSVKG 17

## RESULT 12

US-08-545-809A-119  
;; Sequence 119, Application US/08545809A  
;; Patent No. 6096878  
;; GENERAL INFORMATION:  
;; APPLICANT: Honjo, Tatsuaki  
;; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE  
;; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME  
;; NUMBER OF SEQUENCES: 145  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson, P.C.  
;; STREET: 225 Franklin Street  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: US  
;; ZIP: 02110-2804  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: Windows95  
;; SOFTWARE: FASTSEQ for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/545,809A  
;; FILING DATE: 27-MAR-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/JP93/00603  
;; FILING DATE: 10-MAY-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Freeman, John W.  
;; REGISTRATION NUMBER: 29,066  
;; REFERENCE/DOCKET NUMBER: 06501/004001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-542-5070  
;; TELEFAX: 617-542-8906  
;; TELEX: 200154  
;; INFORMATION FOR SEQ ID NO: 119:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 117 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-545-809A-119

Query Match 74.0%; Score 71; DB 3; Length 117;  
Best Local Similarity 70.6%; Pred. No. 0.008;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GINMGSTGYADSVKG 17  
DB 69 GVSWMGSRTHYADSVKG 85

## RESULT 13

US-08-545-809A-125  
;; Sequence 125, Application US/08545809A  
;; Patent No. 6096878  
;; GENERAL INFORMATION:  
;; APPLICANT: Honjo, Tatsuaki  
;; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE  
;; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME  
;; NUMBER OF SEQUENCES: 145  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson, P.C.  
;; STREET: 225 Franklin Street  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: US  
;; ZIP: 02110-2804  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: Windows95  
;; SOFTWARE: FASTSEQ for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/545,809A  
;; FILING DATE: 27-MAR-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/JP93/00603  
;; FILING DATE: 10-MAY-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Freeman, John W.  
;; REGISTRATION NUMBER: 29,066  
;; REFERENCE/DOCKET NUMBER: 06501/004001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-542-5070  
;; TELEFAX: 617-542-8906  
;; TELEX: 200154  
;; INFORMATION FOR SEQ ID NO: 125:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 118 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-545-809A-125

Query Match 74.0%; Score 71; DB 3; Length 118;  
Best Local Similarity 81.2%; Pred. No. 0.0081;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 INNMGSTGYADSVKG 17  
DB 70 ISWDGSGTYADSVKG 85

## RESULT 14

US-09-424-840B-18  
;; Sequence 18, Application US/09424840B  
;; Patent No. 6790938  
;; GENERAL INFORMATION:  
;; APPLICANT: Berchtold, Peter  
;; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES  
;; FILING DATE: 1999-12-03  
;; CURRENT APPLICATION NUMBER: US/09/424,840B  
;; PRIOR FILING DATE: 1999-12-03  
;; PRIOR APPLICATION NUMBER: DE 19820663.1  
;; PRIOR FILING DATE: 1998-05-08  
;; PRIOR APPLICATION NUMBER: DE 19755227.7  
;; PRIOR FILING DATE: 1997-12-12  
;; PRIOR APPLICATION NUMBER: DE 19723904.8  
;; PRIOR FILING DATE: 1997-06-06  
;; NUMBER OF SEQ ID NOS: 128  
;; SOFTWARE: Patentin version 3.1  
;; SEQ ID NO 18

LENGTH: 124  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-424-840B-18

Query Match 74.0%; Score 71; DB 4; Length 124;  
Best Local Similarity 70.6%; Pred. No. 0.0085;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 GINWNGSTGYADSVKG 17  
Db 50 GISWDSSTGYADSVKG 66

RESULT 15  
US-07-942-245-24  
Sequence 24, Application US/07942245

Patent No. 5639641  
GENERAL INFORMATION:  
APPLICANT: PEDERSEN, Jan T.  
APPLICANT: SEARLE, Stephen M.J.  
APPLICANT: REES, Anthony R.  
APPLICANT: ROGUSKA, Michael A.  
APPLICANT: GUILD, Braydon C.  
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 522  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrie, Mlon, Zimn, Macpeak & Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: HP 9000/700 workstation  
OPERATING SYSTEM: UNIX  
SOFTWARE: In house  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/942,245  
FILING DATE: 09-SEP-1992  
CLASSIFICATION: 530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-942-245-24

Query Match 70.8%; Score 68; DB 1; Length 117;  
Best Local Similarity 70.6%; Pred. No. 0.021;  
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 GINWNGSTGYADSVKG 17  
Db 50 GISWDSSTGYADSVKG 66

Search completed: April 25, 2005, 21:12:14  
Job time : 3.61973 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 20:22:46 ; Search time 7.51996 Seconds

(without alignments)  
752.325 Million cell updates/sec

Title: US-10-029-926D-115

Perfect score: 96

Sequence: 1 GINWNGSTGYADSVKVG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:\*

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13: /cgn2\_6/prodata/2/pubppa/US10A\_PUBCOMB.pep:\*

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20: /cgn2\_6/prodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	96	100.0	17	US-10-032-037B-115
2	96	100.0	17	US-10-029-988B-115
3	96	100.0	17	US-10-032-423A-115
4	96	100.0	17	US-10-029-926B-115
5	96	100.0	17	US-10-194-975-20
6	96	100.0	17	US-10-194-975-20
7	96	100.0	17	US-10-308-817-60
8	96	100.0	17	US-10-032-037B-61
9	96	100.0	17	US-10-029-988B-61
10	96	100.0	17	US-10-032-423A-61
11	96	100.0	17	US-10-453-698-60
12	96	100.0	17	US-10-029-926B-61
13	96	100.0	17	US-10-379-392-21
				US-10-884-830-599

14	96	100.0	122	US-10-447-331-6	Sequence 6, Appl1
15	96	100.0	239	US-09-880-748-937	Sequence 937, App
16	96	100.0	239	US-09-880-748-2015	Sequence 2015, Ap
17	96	100.0	239	US-09-880-748-2038	Sequence 2038, Ap
18	96	100.0	239	US-10-293-418-937	Sequence 937, App
19	96	100.0	239	US-10-293-418-2015	Sequence 2015, Ap
20	96	100.0	239	US-10-293-418-2038	Sequence 2038, Ap
21	96	100.0	242	US-10-935-290-130	Sequence 130, App
22	96	100.0	244	US-10-322-673-42	Sequence 42, Appl1
23	96	100.0	249	US-10-935-290-40	Sequence 40, Appl1
24	96	100.0	266	US-10-032-037B-204	Sequence 204, App
25	96	100.0	266	US-10-029-988B-204	Sequence 204, App
26	96	100.0	266	US-10-032-423A-204	Sequence 204, App
27	96	100.0	277	US-10-032-037B-25	Sequence 25, Appl1
28	96	100.0	277	US-10-032-037B-203	Sequence 203, App
29	96	100.0	277	US-10-029-988B-25	Sequence 25, Appl1
30	96	100.0	277	US-10-029-988B-203	Sequence 203, App
31	96	100.0	277	US-10-032-423A-25	Sequence 25, Appl1
32	96	100.0	277	US-10-032-423A-203	Sequence 203, App
33	96	100.0	277	US-10-029-926B-25	Sequence 25, Appl1
34	96	100.0	277	US-10-029-926B-203	Sequence 203, Appl1
35	96	100.0	280	US-10-880-922-5	Sequence 5, Appl1
36	96	100.0	280	US-10-880-922-6	Sequence 6, Appl1
37	96	100.0	280	US-10-880-922-55	Sequence 55, Appl1
38	96	100.0	280	US-10-880-922-56	Sequence 56, Appl1
39	96	100.0	280	US-10-880-922-60	Sequence 60, Appl1
40	96	100.0	280	US-10-880-922-61	Sequence 61, Appl1
41	96	100.0	309	US-10-052-798-9	Sequence 9, Appl1
42	96	100.0	309	US-10-288-917-9	Sequence 9, Appl1
43	96	100.0	309	US-10-423-448-9	Sequence 9, Appl1
44	96	100.0	444	US-10-032-037B-26	Sequence 26, Appl1
45	96	100.0	464	US-10-029-988B-26	Sequence 26, Appl1

#### ALIGNMENTS

RESULT 1

US-10-032-037B-115

Sequence 115, Application US/10032037B

Publication No. US20040001822A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

TITLE OF INVENTION: MOETIFES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

FILE REFERENCE: 10793/44

CURRENT APPLICATION NUMBER: US/10/032.037B

PRIOR FILING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 115

LENGTH: 17

TYPE: PRT

ORGANISM: Homo sapiens

US-10-032-037B-115

Query Match 100.0%; Score 96; DB 15; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.8e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GINWNGSTGYADSVKVG 17

1 GINWNGSTGYADSVKVG 17

RESULT 2

US-10-029-988B-115

Sequence 115, Application US/10029988B

Publication No. US20040001839A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

```

; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-115

Query Match          100.0%; Score 96; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GINWNGSGTGYADSVKG 17
Db      1 GINWNGSGTGYADSVKG 17

RESULT 3
US-10-032-423A-115
; Sequence 115, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-115

Query Match          100.0%; Score 96; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GINWNGSGTGYADSVKG 17
Db      1 GINWNGSGTGYADSVKG 17

RESULT 4
US-10-029-926B-115
; Sequence 115, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-115
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Query Match          100.0%; Score 96; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GINWNGSGTGYADSVKG 17
Db      1 GINWNGSGTGYADSVKG 17

RESULT 5
US-10-194-975-20
; Sequence 20, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-20

Query Match          100.0%; Score 96; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GINWNGSGTGYADSVKG 17
Db      50 GINWNGSGTGYADSVKG 66

RESULT 6
US-10-308-817-60
; Sequence 60, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rothen, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; PRIOR FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-60

Query Match          100.0%; Score 96; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GINWNGSGTGYADSVKG 17
Db      50 GINWNGSGTGYADSVKG 66

RESULT 7
US-10-032-037B-61
; Sequence 61, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
US-10-032-037B-61
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Query Match          100.0%; Score 96; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GINNNGSGTGYADSVKG 17
        |||||15|||||
Db       50 GINNNGSGTGYADSVKG 66

RESULT 12
US-10-379-392-21
; Sequence 21. Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan

```

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; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Nahiyat, Basail I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US/10/379,392
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-392-21
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Query Match          100.0%; Score 96; DB 16; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GINWNGSTGYADSVKG 17
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Db      50 GINWNGSTGYADSVKG 66
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RESULT 13
US-10-884-830-599
; Sequence 599, Application US/10884830
; Publication No. US2005004354A1
; GENERAL INFORMATION:
; APPLICANT: Jochem, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/10/884,830
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US/09/534,717
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/126,603
; PRIOR FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 599
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-830-599
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Query Match          100.0%; Score 96; DB 16; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 GINWNGSTGYADSVKG 17
      |||||
Db      50 GINWNGSTGYADSVKG 66
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RESULT 14
US-10-447-331-6
; Sequence 6, Application US/10447331
; Publication No. US20030219434A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Ridgway, John B.
; TITLE OF INVENTION: ANTIBODIES FOR CANCER THERAPY AND
; FILE REFERENCE: GENENT.122A
; CURRENT APPLICATION NUMBER: US/10/447,331
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US/09/515,825
; PRIOR FILING DATE: 2000-02-29
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; PRIOR APPLICATION NUMBER: 60/122262
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-331-6
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Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GINWNGSTGYADSVKG 17
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Db      50 GINWNGSTGYADSVKG 66
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RESULT 15
US-09-880-748-937
; Sequence 937, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly's
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 937
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-937
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Query Match          100.0%; Score 96; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GINWNGSTGYADSVKG 17
      |||||
Db      50 GINWNGSTGYADSVKG 66
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 19:57:16 ; Search time 1.96009 Seconds  
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Title: US-10-029-926D-115

Perfect score: 96  
Sequence: 1 GINMNGSTGYADSVKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	98	2	S26928 Ig heavy chain V r
2	87	90.6	112	2	PH1654 Ig heavy chain V r
3	79	82.3	98	2	S26927 Ig heavy chain V r
4	79	82.3	121	2	S31104 Ig heavy chain (su
5	79	82.3	128	2	S31595 Ig heavy chain V r
6	76	79.2	123	2	S30532 Ig heavy chain V r
7	74	77.1	121	2	S31118 Ig heavy chain - h
8	73	76.0	100	2	S69896 Ig heavy chain V r
9	71	74.0	98	2	S26934 Ig heavy chain V r
10	71	74.0	98	2	S26929 Ig heavy chain V r
11	71	74.0	120	2	S44111 Ig heavy chain V-D
12	71	74.0	191	2	JL0048 Ig heavy chain V r
13	69	70.8	120	1	GIHDB Ig heavy chain V-I
14	68	70.8	145	2	S11239 Ig heavy chain V r
15	65	67.7	120	2	S31273 Ig heavy chain V r
16	65	67.7	123	2	PC4281 anti-SS-A/Ro 60K p
17	64	66.7	90	2	S24248 Ig heavy chain V r
18	64	66.7	120	2	S26278 Ig heavy chain V r
19	62	64.6	96	2	S20781 Ig heavy chain V r
20	61.5	64.1	97	2	S26935 Ig heavy chain V r
21	61.5	64.1	97	2	S26462 Ig heavy chain V r
22	61.5	64.1	116	2	B28966 Ig heavy chain pre
23	61.5	64.1	116	2	S31110 Ig heavy chain - h
24	61.5	64.1	146	2	I47184 Ig heavy chain var
25	61	63.5	98	2	S26889 Ig heavy chain V r
26	61	63.5	98	2	S54856 Ig heavy chain V r
27	61	63.5	99	2	S24259 Ig heavy chain V r
28	61	63.5	100	2	S24258 Ig heavy chain V r
29	61	63.5	101	2	S24257 Ig heavy chain V r

30	61	63.5	102	2	S24260 Ig heavy chain V r
31	61	63.5	104	2	S24255 Ig heavy chain V r
32	61	63.5	105	2	S24249 Ig heavy chain V r
33	61	63.5	106	2	S24256 Ig heavy chain V r
34	61	63.5	108	2	PH1648 Ig heavy chain V r
35	61	63.5	109	2	S24254 Ig heavy chain V r
36	61	63.5	109	2	S24253 Ig heavy chain V r
37	61	63.5	109	2	PH1649 Ig heavy chain V r
38	61	63.5	110	2	S24250 Ig heavy chain V r
39	61	63.5	112	2	PH1647 Ig heavy chain V r
40	61	63.5	113	2	S24247 Ig heavy chain V r
41	61	63.5	115	2	S09382 Ig heavy chain - c
42	61	63.5	117	2	A45953 Ig heavy chain pre
43	61	63.5	118	2	S31121 Ig heavy chain - h
44	61	63.5	119	2	D36005 Ig heavy chain V r
45	61	63.5	119	2	S31107 Ig heavy chain - h

#### ALIGNMENTS

RESULT 1  
S26928  
Ig heavy chain V region (DP-32) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S26928  
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of  
A/Reference number: S26985; MUID:93021117; PMID:1404388  
A/Accession: S26928  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-98 <TOM>  
A/Cross-references: EMBL:212334; NID:G32887; PIDN:CAA78204.1; PID:G32888  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 96; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINMNGSTGYADSVKG 17  
DB 50 GINMNGSTGYADSVKG 66

#### RESULT 2

PH1654  
Ig heavy chain V region (clone 6H9) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
C/Accession: PH1654  
R/Hillson, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Sasso, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphy-  
A/Reference number: PH1642; MUID:9301610; PMID:8315388  
A/Molecule type: mRNA  
A/Residues: 1-112 <HIL>  
A/Experimental source: B cell  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 90.6%; Score 87; DB 2; Length 112;  
Best Local Similarity 94.1%; Pred. No. 4.4e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GINMNGSTGYADSVKG 17  
|||||

Db 42 GINWNGSTGYADSVKG 58

RESULT 3

Ig heavy chain V region (DP-31) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S26927  
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
A/Reference number: S26885; MUID:93021117; PMID:1404388  
A/Accession: S26927  
A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1-98 <TOM>  
A/Cross-references: EMBL:Z12333; NID:932885; PDB:CAA78203.1; PID:932886  
C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 79; DB 2; Length 98;  
Best Local Similarity 82.4%; Pred. No. 6.2e-05;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GINWNGSTGYADSVKG 17  
||:|||||  
Db 50 GISMNGSITGYADSVKG 66

RESULT 4

S31104  
Ig heavy chain (subclass IgM) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 23-Jul-1999  
C/Accession: S31104  
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmat  
Eur. J. Immunol. 22, 247-251, 1992  
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A/Reference number: S31104; MUID:92111633; PMID:170252  
A/Accession: S31104  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-121 <RAA>  
A/Cross-references: EMBL:X63080; NID:932846; PDB:CAA44802.1; PID:932647  
C/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 79; DB 2; Length 121;  
Best Local Similarity 82.4%; Pred. No. 7.7e-05;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GINWNGSTGYADSVKG 17  
||:|||||  
Db 50 GISMNGSITGYADSVKG 66

RESULT 5

S31595  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31595  
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31595  
A/Status: preliminary  
A/Molecule type: mRNA

A/Residues: 1-128 <CUI>  
A/Cross-references: EMBL:Z14171; NID:931007; PDB:CAA78540.1; PID:931008  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/23-106/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 79; DB 2; Length 128;  
Best Local Similarity 82.4%; Pred. No. 8.1e-05;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GINWNGSTGYADSVKG 17  
||:|||||  
Db 58 GISMNGSITGYADSVKG 74

RESULT 6

S30532  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S30532  
R/Mariette, X.  
submitted to the EMBL Data Library, October 1992  
A/Reference number: S30520  
A/Accession: S30532  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-123 <MAR>  
A/Cross-references: UNIPROT:Q8MU38; EMBL:Z18318  
C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 76; DB 2; Length 123;  
Best Local Similarity 76.5%; Pred. No. 0.00022;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GINWNGSTGYADSVKG 17  
||:|||||  
Db 50 GISMNGSITGYADSVKG 66

RESULT 7

S31118  
Ig heavy chain - human  
C/Species: Homo sapiens (man)  
C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C/Accession: S31118  
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmat  
Eur. J. Immunol. 22, 247-251, 1992  
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A/Reference number: S31104; MUID:92111633; PMID:170252  
A/Accession: S31118  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-121 <RAA>  
A/Cross-references: EMBL:X62969  
C/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 74; DB 2; Length 121;  
Best Local Similarity 76.5%; Pred. No. 0.00044;  
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GINWNGSTGYADSVKG 17  
||:|||||  
Db 50 GISMNGSITGYADSVKG 66

RESULT 8

S69896

Ig heavy chain/region (clone RFKL5H), rheumatoid factor - human  
C:Species: Homo sapiens (man)  
C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
C:Accession: S69896  
R:Randem, I., Pascual, V., Victor, K., Thompson, K.M., Forre, O., Capra, D.J., Natvig, J.  
Eur. J. Immunol. 23, 1220-1225, 1993  
A>Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune response  
A:Reference number: S69896; MUID:93272805; PMID:8500520  
A:Accession: S69896  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-100 <RAN>  
A:Cross-references: EMBL:X73605; NID:G509797; PION:CA5198.1; PID:G509798  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology <IMM>  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match	76.0%;	Score 73;	DB 2;	Length 100;
Best Local Similarity	76.5%;	Pred. No. 0.00051;		
Matches 13; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

QY 1 GINWNGSTGYADSVKG 17  
||| |||||  
Db 50 GITWNSGRIGYADSVKG 66

## RESULT 9

Ig heavy chain V region (DP-59) - human (fragment)  
C|Species: Homo sapiens (man)  
C|Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C|Accession: S26934  
R|Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A|Title: The repertoire of human germline V(H) sequences reveals about fifty groups of  
A|Reference number: S26985; MUID:93021117; PMID:1404388  
A|Accession: S26934  
A|Status: preliminary  
A|Molecule type: DNA  
A|Reads: 1-98 <TOM>  
A|Cross-references: EMBL:Z12359; NID:G32937; PIDN:CAA78229.1; PID:G32938  
C|Superfamily: immunoglobulin V region; immunoglobulin homology  
C|Keywords: heterotetramer; immunoglobulin  
P15-98/Domain: immunoglobulin homology <IMM>

Query Match	74.0%;	Score 71;	DB 2;	Length 98;
Best Local Similarity	70.6%;	Pred. No. 0.001;		
Matches 12;	Conservative 2;	Mismatches 3;	Indels 0;	Gaps 0;

```
QY      1 GINWNGSTGYADSVKG 17
      |::||| | |||||
Db      50 GVSWNGSRTHYADSVKG 66
```

## RESULT 10

Ig heavy chain V region (DP-33) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S26929  
 R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
 J. Mol. Biol. 227, 776-798, 1992  
 A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V  
 A:Reference number: S26985; MUID:9302117; PMID:1404388  
 A:Accession: S26929  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-98 <TOM>  
 A:Cross-references: EMBL:Z12335; NID:G32869; PIND:CAA78205.1; PID:G32890  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 71; DB 2; Length 98;

Best Local Similarity 81.2%; Pred. NO. 0.001;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
QY      2 INWNGSTGYADSVKG 17
      |:|:|||||
Db      51 ISWDGGSTYYADSVKG 66
```

## RESULT 11

Ig heavy chain V-D-J region - human  
C.Species: Homo sapiens (man)  
C.Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C.Accession: S4411  
R.Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A.Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable  
A.Reference number: S44105  
A.Accession: S4411  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-120 <HAN>  
A.Cross-references: EMBL:Z31387; NID:G472965; PIDD:CA83262.1; PID:G940522  
C.Superfamily: immunoglobulin V region: immunoglobulin homology  
C.Keywords: heterotetramer; immunoglobulin  
F.15-98/Domain: immunoglobulin homology <IMM>

Query Match	74.0%	Score 71;	DB 2;	Length 120;
Best Local Similarity	81.2%	Pred. No. 0.0012;		
Matches 13; Conservative	2;	Mismatches 1;	Indels 0;	Gaps 0;

```
QY      2 INMNGSTGYADSVKG 17
      |:|:|||||
Db      51 ISWDGGSTYYADSVKG 66
```

## RESULT 12

Ig heavy chain V region precursor (clone CR19) - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 15-Mar-2004  
C:Accession: J10048; S66433  
R:Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.  
J. Exp. Med. 167, 2011-2016, 1988  
A:Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new  
A:Reference number: J10047; MUID:88258392; PMID:3133445  
A:Accession: J10048  
A:Molecule type: mRNA  
A:Residues: 1-191 <BBA>  
A:Note: the authors translated the reading frame which extends to the stop codon; the s  
A:Note: this sequence belongs to the VH III subgroup  
R:Muller-Newen, G.; Koehne, C.; Keul, R.; Hermann, U.; Mueller-Esterl, W.; Wijdenes, J  
Eur. J. Biochem. 236, 837-842, 1996  
A:Title: Purification and characterization of the soluble interleukin-6 receptor from h  
A:Reference number: S66433; MUID:96270733; PMID:8665902  
A:Accession: S66433  
A:Molecule type: protein  
A:Residues: 9-18 <MNU>  
C:Keywords: heterotrimer; immunoglobulin  
#23-106/Domain: immunoglobulin homology <IMM>

Query Match	74.0%;	Score 71;	DB 2;	Length 191;
Best Local Similarity	70.6%;	Pred. No. 0.002;		
Matches 12;	Conservative 2;	Mismatches 3;	Indels 0;	Gaps 0;

QY 1 GINWNGSTGYADSVKG 17  
|::||| | |||||  
Db 58 GVSWNGSRTHYADSVKG 74

## RESULT 13

Ig heavy chain V-III region (Dob) - human

C:Species: Homo sapiens (man)  
 C:Date: 31-Dec-1979 #sequence\_revision 31-Dec-1979 #text\_change 09-Jul-2004  
 C:Accession: A90431; A02065  
 R:Steiner, L.A.; Garcia Pardo, A.; Margolies, M.N.  
 Biochemistry 18, 4068-4080, 1979  
 A:Title: Amino acid sequence of the heavy-chain variable region of the crystallizable hu  
 A:Reference number: A90431; PMID:80020921; PMID:114209  
 A:Accession: A90431  
 A:Molecule type: protein  
 A:Residues: 1-120 <STR>  
 A:Cross-references: UNIPROT:P01782  
 R:Steiner, L.A.; Lopes, A.D.  
 Biochemistry 18, 4054-4067, 1979  
 A:Title: The crystallizable human myeloma protein Dob has a hinge-region deletion.  
 A:Reference number: A90430; PMID:80020920; PMID:114208  
 A:Contents: annotation  
 A>Note: this gamma-1 myeloma protein has a deletion in the hinge region; there are no 14  
 C:Genetics:  
 A:Gene: CDB:IGHV@  
 A:Cross-references: GDB:128528; OMIM:147070  
 A:Map position: 14q32.33-14q32.33  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>  
 F:22-96/Disulfide bonds: #status predicted

Query Match 71.9%; Score 69; DB 1; Length 120;  
 Best Local Similarity 81.2%; Pred. No. 0.0025;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GINMGSGTGYADSVKG 17  
 |||:| |||||  
 DB 51 ITWNGSVLYADSVKG 66

RESULT 14  
 S11239  
 Ig heavy chain V region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S11239  
 R:Felgenhauer, M.; Kohl, J.; Rueker, F.  
 Nucleic Acids Res. 18, 4927, 1990  
 A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of  
 A:Reference number: S11239; MUID:90370490; PMID:1697678  
 A:Accession: S11239  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-145 <PEL>  
 A:Cross-references: EMBL:X53613; NID:923865; PIDN:CAA37675.1; PID:9762936  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 68; DB 2; Length 145;  
 Best Local Similarity 70.8%; Pred. No. 0.0042;  
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GINMGSGTGYADSVKG 17  
 |||:| |||||  
 DB 69 GISWSSSIGYADSVKG 85

RESULT 15  
 S36273  
 Ig heavy chain V region (clone alpha-THY-32) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 23-Jul-1999  
 C:Accession: S36273  
 R:Giffiths, A.D.; Malmqvist, M.; Marts, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
 EMBO J. 12, 725-734, 1993  
 A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
 A:Reference number: S36256; MUID:91178448; PMID:7679990

A:Accession: S36273  
 A>Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-120 <GRI>  
 A:Cross-references: EMBL:Z18834; NID:933116; PIDN:CAA79286.1; PID:9939896  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.7%; Score 65; DB 2; Length 120;  
 Best Local Similarity 76.5%; Pred. No. 0.0099;  
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GINMGSGTGYADSVKG 17  
 |||:| |||||  
 DB 50 GISNNGSIGYADSVKG 66

Search completed: April 25, 2005, 20:24:11  
 Job time : 2.96009 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:10:00 ; Search time 8.78271 Seconds

(without alignments)  
991.192 Million cell updates/sec

Title: US-10-029-926D-115

Perfect score: 96

Sequence: 1 GINWNGSTGYADSVK 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	112	2	Q9HCC1
2	84	87.5	499	2	Q8NSK4
3	82	85.4	494	2	Q6ZW64
4	79	82.3	104	2	Q9UL87
5	73	76.0	573	2	Q8WU38
6	69	71.9	472	2	Q6N089
7	61.5	64.1	120	1	HV3U_HUMAN
8	61.5	64.1	116	1	HV05_CARAU
9	61	63.5	121	2	Q9UL71
10	61	63.5	593	2	Q6INM5
11	61	63.5	597	2	Q96B89
12	61	63.5	614	2	Q6DDQ7
13	60	62.5	584	2	Q6INK3
14	59	61.5	117	1	HV53_MOUSE
15	59	61.5	493	2	Q6GKX2
16	57	59.4	117	1	HV3C_HUMAN
17	56	58.3	118	2	Q9UL72
18	55	57.3	479	2	Q91WP5
19	54.5	56.8	466	2	Q6INW8
20	54	56.2	112	2	Q9UGP3
21	53	55.2	115	1	HV3F_HUMAN
22	52	54.2	493	2	Q68CN4
23	51	53.1	121	1	HV3J_HUMAN
24	51	53.1	469	2	Q9FDT2
25	51	53.1	475	2	Q6MZ06
26	51	53.1	838	2	Q7UV9
27	50.5	52.6	97	1	HV56_MOUSE
28	50	52.1	874	2	Q6C6K4
29	49	51.0	767	2	Q9U234
30	49	51.0	1089	2	Q64U63
31	48.5	50.5	117	1	HV02_CANFA

32	48	50.0	99	2	Q6B743	Q6B743	oryctolagus
33	48	50.0	117	1	HV55_MOUSE	P18526	mus musculus
34	48	50.0	119	1	HV31_HUMAN	P01773	homo sapien
35	48	50.0	279	2	Q9WZ18	Q9WZ18	thermoptoga
36	48	50.0	298	2	Q9XGB4	Q9XGB4	trifolium
37	48	50.0	416	2	Q9NPP6	Q9NPP6	homo sapien
38	48	50.0	469	2	Q8PD28	Q8PD28	xanthomonas
39	48	50.0	473	2	Q91205	Q91205	mus musculus
40	48	50.0	475	2	Q6GWM7	Q6GWM7	homo sapien
41	48	50.0	654	2	Q8FAX3	Q8FAX3	dictyosteli
42	48	50.0	761	2	Q20898	Q20898	caenorhabdi
43	48	50.0	4342	2	Q91157	Q91157	pseudomonas
44	47.5	49.5	100	2	Q6B755	Q6B755	oryctolagus
45	47	49.0	87	2	Q7Y3K4	Q7Y3K4	enterobacte

#### ALIGNMENTS

RESULT 1	PRELIMINARY	PRT	112 AA.
ID Q9HCC1			
AC Q9HCC1			
DT 01-MAR-2001 (TREMBlrel. 16, Created)			
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)			
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)			
DE Single chain Fv (Fragment).			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX NCBI_Taxid=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;			
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AB049915; BAB16829.1; -			
DR HSSP; P01783; 1IGC.			
DR InterPro; IPR007110; IG-Like.			
DR SMART; SM00406; IGV; 1.			
DR PROSITE; PSS0835; IG-LIKE; 1.			
FT NON TER			
FT NON TER			
FT NON TER			
SQ SEQUENCE 112 AA; 12243 MW; 24F1A45ECB84788 CRC64;			
Query Match	100.0%;	Score 96;	DB 2; Length 112;
Best Local Similarity	100.0%;	Pred. No. 4.8e-07;	
Matches 17; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	GINWNGSTGYADSVK 17	
DB	50	GINWNGSTGYADSVK 66	
RESULT 2			
ID Q8NSK4			
AC Q8NSK4			
DT 01-OCT-2002 (TREMBlrel. 22, Created)			
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)			
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)			
DE MGC27165 protein.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX NCBI_Taxid=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Blood;			
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA Krausner R.D., Collins F.S., Wagner L., Shennan C.M., Schlier G.D.,			
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.;			

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusita K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loggellano N.A., Peters G.U., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.O., McKernan K.J., Malek J.R., Gunaratne P.H.,  
 RA Richard S., Wotley K.C., Hale S., Garcia A.M., Gay L.U., Huily S.W.,  
 RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzyanski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Blood;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC032249; AAH32249.1; -.  
 DR HSSP: P01876; 10W0.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig-cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF07654; C1-set; 2.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IG; 1.  
 DR PROSITE: PSS0835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN 1.  
 SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;  
 QY  
 Db 2 INNMGGSTGYADSVK 17  
 70 INNMGGSTGYADSVK 85  
 Query Match 87.5%; Score 84; DB 2; Length 499;  
 Best Local Similarity 93.8%; Pred. No. 0.00017;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 RESULT 3  
 Q6ZW64 PRELIMINARY; PRT; 494 AA.  
 ID Q6ZW64  
 AC Q6ZW64  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein FLJ41552.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.,  
 RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,  
 RA Isono Y., Kawai Hio Y., Saito K., Nishikawa T., Kimura K.,  
 RA Yamaehita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
 RA Magatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,  
 RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,  
 RA Masuno Y., Nagai K., Isogai T.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK123546; BAC85641.1; -.  
 DR HSSP: P01842; 1A0X.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig-cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 RP SEQUENCE FROM N.A.

DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF07654; C1-set; 2.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00409; IG; 4.  
 DR SMART: SM00407; IGcl; 2.  
 DR SMART: SM00406; IGv; 1.  
 DR PROSITE: PSS0835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN 1.  
 SQ SEQUENCE 494 AA; 53321 MW; CD8140B37A23A882 CRC64;  
 QY  
 Db 1 GINMGGSTGYADSVK 17  
 69 GIDMGGDAGYADSVK 85  
 Query Match 85.4%; Score 82; DB 2; Length 494;  
 Best Local Similarity 82.4%; Pred. No. 0.00034;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 RESULT 4  
 Q9UL87 PRELIMINARY; PRT; 104 AA.  
 ID Q9UL87  
 AC Q9UL87  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjlin.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL: AF035027; AAD56263.1; -.  
 DR HSSP: P01810; 2FBU.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_v.  
 DR SMART: SM00406; IGv; 1.  
 DR PROSITE: PSS0835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 104 AA; 11598 MW; 611D1A3F40E96E7B CRC64;  
 Query Match 82.3%; Score 79; DB 2; Length 104;  
 Best Local Similarity 82.4%; Pred. No. 0.0002;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY  
 Db 1 GINMGGSTGYADSVK 17  
 29 GISMGGSTGYADSVK 45  
 RESULT 5  
 Q8WU38 PRELIMINARY; PRT; 573 AA.  
 ID Q8WU38  
 AC Q8WU38  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.



RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toohyuk S., Caramici P., Prange C.,  
RA Reha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,  
RA Krzywiński M.I., Skalka U., Smallue D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Primary B-Cells;  
RC Straubeberg R.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BCO21276; AAI21276.1; -.  
DR PIR: S21205; S21205.  
DR PIR: S30532; S30532.  
DR HSSP: P18529; 118K.  
DR Pfam: PF07654; Cl-sect; 2.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; Ig; 1.  
DR PROSITE: PS50835; IG\_LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
DR Hypothetical protein.  
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match 82.3%; Score 79; DB 2; Length 573;  
Best Local Similarity 82.4%; Pred. No. 0.0011;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSTGYADSVKG 17  
Db 69 GISWNGSVIYADSVKG 85

RESULT 6  
ID Q6N089 PRELIMINARY; PRT; 472 AA.  
AC Q6N089;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686P15220.  
GN Name=DKFZp686P15220;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Wambut R., Heubner D., Mewes H.W., Weil B., Amlid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BX640627; CA545781.1; -.  
DR HSSP: P01861; 1ADQ.  
DR InterPro: IPR003599; Ig.  
DR InterPro: IPR007110; Ig-1like.  
DR InterPro: IPR003597; Ig-cl.

DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF07654; Cl-sect; 3.  
DR SMART: SM00409; Ig; 2.  
DR SMART: SM00407; Igcl; 3.  
DR SMART: SM00406; Ig; 1.  
DR PROSITE: PS50835; IG\_LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
DR Hypothetical protein.  
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 76.0%; Score 73; DB 2; Length 472;  
Best Local Similarity 76.5%; Pred. No. 0.0081;  
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GINWNGSTGYADSVKG 17  
Db 69 GISWNGSVIYADSVKG 85

RESULT 7  
ID HV3U\_HUMAN STANDARD; PRT; 120 AA.  
AC P01782;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Ig heavy chain V-III region DOB.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=80020921; PubMed=114209;  
RA Steiner L.A., Garcia Pardo A., Margolies M.N.;  
RT "Amino acid sequence of the heavy-chain variable region of the  
crystallizable human myeloma protein Dob.";  
RL Biochemistry 18:4068-4080(1979).  
RN [2]  
RP CRYSTALLIZATION.  
RX MEDLINE=80020920; PubMed=114208;  
RA Steiner L.A., Lopes A.D.;  
RT "The crystallizable human myeloma protein Dob has a hinge-region  
deletion.";  
RL Biochemistry 18:4054-4067(1979).  
CC -I- MISCELLANEOUS: This gamma-1 myeloma protein has a deletion in the  
hinge region. There are no light-heavy or inter-heavy chain  
disulfide bonds.  
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.  
DR PIR: A90431; GIHDB.  
DR HSSP: P01772; 2F84.  
DR GO: GO:0005576; C:extracellular; NAS.  
DR GO: GO:0003823; F:antigen binding; NAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro: IPR007110; Ig-1like.  
DR InterPro: IPR003596; Ig\_V.  
DR SMART: SM00407; Ig; 1.  
DR Pfam: PF00047; Ig; 1.  
DR PROSITE: PS50835; IG\_LIKE; 1.  
DR Direct protein sequencing; Immunoglobulin V region.  
FT DOMAIN 1 112  
FT NON\_TER 120 120  
SQ SEQUENCE 120 AA; 13440 MW; 880DDE307C4B2627 CRC64;

Query Match 71.9%; Score 69; DB 1; Length 120;  
Best Local Similarity 81.2%; Pred. No. 0.0083;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 INWNGSTGYADSVKG 17  
Db 51 ITWNGSVIYADSVKG 66



DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 5.

DR Pfam; PF07654; C1-set; 4.  
DR Pfam; PF00047; iq; 3.

DR SMART; SM00409; IG; 4.  
DR SMART; SM00407; IG1; 4.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_4.  
DR PROSITE; PS00678; WD\_REPEATS\_1; UNKNOWN\_1.  
SQ SEQUENCE 614 AA; 68253 MW; 2631B7CF955270C0 CRC64;

Query Match 63.5%; Score 61; DB 2; Length 614;  
Best Local Similarity 56.5%; Pred. No. 0.78;  
Matches 13; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 1 GINW-----NGSGTGYADSVKG 17  
Db 61 GLOWSVISDGGSTYADSVKG 83

## RESULT 13

ID O6INK3 PRELIMINARY; PRT; 584 AA.  
AC O6INK3;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenodidae; Xenopus.  
NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedlin T.B., Toehiyki S., Carninci P., Prange C.,  
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakeley M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,  
RA Krzywiński M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Straube R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
Initiative";  
RL Dev. Dyn. 225:384-391(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Klein S., Straube R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC072277; AAH72277.1; --  
DR HSSP; P01842; IAOK.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.

DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; Cl-sec; 2.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00409; IG; 4.  
DR SMART; SM00407; IG1; 4.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KM Hypothetical protein.  
SQ SEQUENCE 584 AA; 64449 MW; F1349DD169FD64 CRC64;

Query Match 62.5%; Score 60; DB 2; Length 584;  
Best Local Similarity 56.5%; Pred. No. 1.1;  
Matches 13; Conservative 1; Mismatches 3; Indels 6; Gaps 1;

QY 1 GINW-----NGSGTGYADSVKG 17  
Db 63 GLOWSVISDGGSTYADSVKG 85

## RESULT 14

ID HV53 MOUSE STANDARD; PRT; 117 AA.  
AC P18524;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region RF precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BA1B/CJ;  
RX MEDLINE=99279149; PubMed=2499654;  
RA Levy N.S., Malpieiro U.V., Lebecque S.G., Gearhart P.J.;  
RT "Early onset of somatic mutation in immunoglobulin VH genes during the  
primary immune response";  
RL J. Exp. Med. 169:2007-2019(1989).  
CC -1- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.  
DR PIR; J0503; HVMSRF.  
DR HSSP; P18529; 118K.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KM Hybridoma; Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117  
FT DOMAIN 20 49  
FT DOMAIN 50 54  
FT DOMAIN 55 68  
FT DOMAIN 69 85  
FT DOMAIN 86 117  
FT DISULFID 41 115  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 61.5%; Score 59; DB 1; Length 117;  
Best Local Similarity 75.0%; Pred. No. 0.29;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 INNWGSGTGYADSVKG 17  
Db 70 INNSGSTRSDGTYADSVKG 85

RESULT 15  
Q6GMX2 PRELIMINARY; PRT; 493 AA.

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AC O6GMX2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lotteliello N.A., Peters G.J., Abramson R.D., Mullenbach S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhe D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RC Strausberg R.;
RX EMBL: BC073771; AAT73771.1; -.
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF07654; Cl-set; 2.
DR Pfam: PF0047; IG; 3.
DR SMART: SM00409; IG; 4.
DR SMART: SM00407; IGC1; 2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG-LIKE; 4.
DR PROSITE: PS00230; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 493 AA; 52865 MW; 55B999305B286203 CRC64;

Query Match 61.5%; Score 59; DB 2; Length 493;
Best Local Similarity 75.0%; Pred. No. 1.3;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 INNNGSGTGYADSVKG 17
| : || || || ||
DB 70 INSDGSGTGYADSVKG 85

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Search completed: April 25, 2005, 20:34:03  
 Job time : 9.78271 secs

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XX  
SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6  
1 MRAPVI 6

RESULT 2  
ABG78133  
ID ABG78133 standard; peptide; 6 AA.

XX AC ABG78133;  
XX DT 15-NOV-2002 (first entry)

XX DE Human Fv molecule hypervariable region related peptide #8.

XX KW Human; Fv molecule; hypervariable region; single chain Fv; cyrostatic;  
XX KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
XX KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX OS Homo sapiens.

XX PN WO00259264-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US049440.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;

XX PI Plakain D, Peretz T;

XX DR WPI; 2002-619166/66.

XX PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
PT or fragment, or construct of fragment with enhanced binding  
PT characteristics so as to selectively bind target cell in favor of other  
PT cells.

XX PS Claim 2; Page 76; 232pp; English.

XX CC The invention relates to a peptide or polypeptide comprising an Fv  
CC molecule, a construct or fragments or a construct of a fragment with  
CC enhanced binding characteristics which selectively and/or specifically  
CC binds to a target cell in favour of other cells, where binding is  
CC primarily determined by a first hypervariable region and Fv is a single  
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
CC association with or attached, coupled, combined, linked or fused to a  
CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
CC the medicament has activity against a diseased cell, preferably a cancer  
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
CC composition for use in inhibiting the growth of a diseased or cancer  
CC cell. This sequence represents a human Fv molecule hypervariable region  
CC related peptide of the invention

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6

Db 1 MRAPVI 6

RESULT 3  
ABG91824  
ID ABG91824 standard; peptide; 6 AA.

XX AC ABG91824;

XX DT 04-DEC-2002 (first entry)

XX DE Human antibody fragment #8.

XX KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
XX KW metastasis; hypervariable region; autoimmune disease; thrombosis;  
XX KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
XX KW myocardial infarction; retinopathic disease; abnormal platelet function;  
XX KW sulphated tyrosine-dependent protein-protein interaction.

XX OS Homo sapiens.

XX PN WO00253700-A2.

XX PD 11-JUL-2002.

XX PF 31-DEC-2001; 2001WO-US049442.

XX PR 29-DEC-2000; 2000US-00751181.

XX PR 29-DEC-2000; 2000US-0258948P.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Max-Haim H;

XX PI Santhanon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX DR WPI; 2002-674776/72.

XX PT Novel isolated epitope present on cancer cells and important in  
PT physiological phenomena such as cell rolling, metastasis and  
PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
PT diseases, and cancer.

XX PS Claim 1; Page 228; 0pp; English.

XX CC The invention relates to an isolated epitope present on cancer cells and  
CC important in physiological phenomena such as cell rolling, metastasis and  
CC inflammation, where the epitope is capable of being bound by an antibody,  
CC its antigen-binding fragment or its complex comprising at least one  
CC antibody or its binding fragment having a first hypervariable region. The  
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
CC mortality of tumour or leukaemia cells, for increasing the susceptibility  
CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
CC leukaemia agents, or for decreasing the number of tumour or leukaemia  
CC cells in a patient, or in the manufacture of a medicament for the above  
CC mentioned purposes. The epitopes are useful for diagnosing and treating  
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
CC diseases, cardiovascular diseases such as myocardial infarction,  
CC retinopathic diseases and other diseases mediated by abnormal platelet  
CC function and diseases caused by sulphated tyrosine-dependent protein-  
CC protein interactions. This sequence represents a human antibody fragment  
CC of the invention

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



OY 1 MRAPVI 6  
 DB 1 MRAPVI 6

RESULT 4  
 ID ADI28369 standard; peptide; 6 AA.

XX ADI28369;

XX 06-MAY-2004 (first entry)

XX Human CDR3 peptide, used in therapeutic composition.

XX Human: antibody; scFv; complementarity determining region; drug delivery;  
 cancer; therapy.

XX Homo sapiens.

XX MO2004002528-AA.

XX 08-JAN-2004.

XX 30-JUN-2003; 2003MO-US020604.

XX 01-JUL-2002; 2002US-00189025.

XX (SAVI-) SAVIENT PHARM INC.

XX Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;

XX WPI; 2004-099189/10.

XX Composition comprising an agent and/or antibody or its fragment, useful  
 for treating auto-immune disease, thrombosis, restenosis, metastasis, or  
 for inhibiting growth and/or replication of tumor cells or leukemia  
 cells.

XX Claim 14; SEQ ID NO 4; 58pp; English.

XX The present sequence is that of a human antibody complementarity  
 determining region 3 (CDR3). The invention relates to compositions  
 utilising an agent and an antibody or its fragment. The agent is a toxin,  
 radioisotope or pharmaceutical agent such as doxorubicin. It is complexed  
 or combined with or conjugated to the antibody or its fragment. The  
 antibody may have a first hypervariable region comprising the present  
 sequence. The agent and/or antibody can be present in the composition is  
 a sub-clinical amount, i.e. less than the amount generally found to be  
 clinically effective when the agent is administered alone. The  
 composition is used in claimed methods of: inhibiting cell rolling,  
 inflammation, thrombosis, restenosis, metastasis, the growth and/or  
 replication of tumour cells or leukemia cells, an increase in number of  
 tumour or leukemia cells, cell-cell, cell-matrix, platelet-matrix,  
 platelet-platelet and/or cell-platelet complex formation, aggregation or  
 adhesion; increasing the mortality rate of tumour or leukemia cells, the  
 susceptibility of disease cells to damage by anti-disease agents, and the  
 susceptibility of tumour or leukemia cells to damage by anti-cancer  
 agents; and ameliorating the effects of a disease, preventing a disease,  
 treating a disease or inhibiting the progress of a disease.

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRAPVI 6  
 DB 1 MRAPVI 6

RESULT 5

ADJ57364  
 ID ADJ57364 standard; peptide; 6 AA.

XX ADJ57364;

XX 06-MAY-2004 (first entry)

XX P-selectin glycoprotein ligand-1-binding scFv antibody fragment L32 CDR3.

XX P-selectin glycoprotein ligand-1; PSG-1; antibody; scFv; cytostatic;  
 antiinflammatory; immunosuppressive; complementarity determining region;  
 human.

XX Homo sapiens.

XX MO2004003166-AA.

XX 08-JAN-2004.

XX 30-JUN-2003; 2003MO-US020602.

XX 01-JUL-2002; 2002US-00189032.

XX (SAVI-) SAVIENT PHARM INC.

XX Levanon A, Ben-Levy R, Plaksin D, Stanton E, Hagai Y;

XX Hoch Mar- Chaim H;

XX WPI; 2004-203378/19.

XX Novel antibody or its fragment that binds to an epitope of P-selectin-  
 glycoprotein ligand-1, useful for diagnosing/prognosing inflammation,  
 infection, auto-immune disease, metastasis, tumor/leukemia cell in  
 patient.

XX Claim 2; SEQ ID NO 2; 106pp; English.

XX The present sequence is that of the heavy chain complementarity  
 determining region 3 (CDR3) of L32 ADJ57363, an scFv antibody fragment  
 that binds P-selectin glycoprotein ligand-1 (PSGL-1). L32 was identified  
 by screening a phage library, which had diversity only in the heavy chain  
 CDR3 regions, against a leukemia cell to select specific antibodies that  
 recognised leukemia cell surface determinants, wherein the specific  
 receptor was not previously known or characterised. The invention relates  
 to an antibody or its fragment having the binding capabilities of L32 and  
 comprising at least one of the heavy chain CDRs of L32. Such antibodies  
 can be used in therapeutic, diagnostic, prognostic and staging methods.  
 Pharmaceutical compositions comprising such antibodies are used to treat  
 conditions related to: inhibiting or treating cell rolling, inflammation,  
 autoimmune disease, infection (e.g. HIV infection), metastasis, and  
 growth and/or replication of tumour cells; increasing the mortality of  
 tumour cells; inhibiting growth and/or replication of tumour cells;  
 inhibiting growth and/or replication of leukemia cells; increasing the  
 mortality rate of leukemia cells; altering the susceptibility of  
 diseased cells to damage by anti-disease agents; increasing the  
 susceptibility of tumour cells to damage by anti-cancer agents;  
 increasing the susceptibility of leukemia cells to damage by anti-  
 leukemia agents; inhibiting increase in number of tumour cells in a  
 patient; decreasing the number of tumour cells in a patient; inhibiting  
 increase in number of leukemia cells in a patient; and decreasing the  
 number of leukemia cells in a patient. Other methods are provided to  
 induce antibody-dependent cell-mediated cytotoxicity or stimulate natural  
 killer or T cells using the antibodies. A method of purging tumour cells  
 from a patient involves incubating the cells with the antibody.

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRAPVI 6  
 DB 1 MRAPVI 6

Db 1 MRAPVI 6

RESULT 6  
ABG78329

ID ABG78329 standard; protein; 246 AA.

XX ABG78329;

DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #204.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytosolic;

XX disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;

XX lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX Homo sapiens.

XX MO200259264-A2.

XX 01-AUG-2002.

XX 31-DEC-2001; 2001WO-US049440.

XX 29-DEC-2000; 2000US-00751181.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;

XX Plaksain D, Peretz T;

XX WPI; 2002-619166/66.

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct

XX PT or fragment, or construct of fragment with enhanced binding

XX PT characteristics so as to selectively bind target cell in favor of other

XX cells.

XX PS Disclosure; Page 44-45; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv

XX molecule, a construct or fragments or a construct of a fragment with

XX enhanced binding characteristics which selectively and/or specifically

XX binds to a target cell in favour of other cells, where binding is

XX primarily determined by a first hypervariable region and Fv is a single

XX chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in

XX association with or attached, coupled, combined, linked or fused to a

XX pharmaceutical agent, is useful in the manufacture of a medicament, where

XX the medicament has activity against a diseased cell, preferably a cancer

XX cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,

XX myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an

XX acute myeloid leukaemia cell). The peptide is also useful for preparing a

XX composition for use in inhibiting the growth of a diseased or cancer

XX cell. This sequence represents a human Fv molecule hypervariable region

XX related peptide of the invention

XX SO Sequence 246 AA;

XX Query Match 100.0%; Score 29; DB 5; Length 246;

XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;

XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 MRAPVI 6

XX Db 100 MRAPVI 105

XX RESULT 7

XX ABG92026

XX ID ABG92026 standard; protein; 246 AA.

XX AC ABG92026;

XX 04-DEC-2002 (first entry)

XX Antibody protein #5.

XX Antibody; epitope; cancer; tumour; cell rolling; inflammation;

XX metastasis; hypervariable region; autoimmune disease; thrombosis;

XX restenosis; leukaemia; inflammatory disease; cardiovascular disease;

XX myocardial infarction; retinopathic disease; abnormal platelet function;

XX sulphated tyrosine-dependent protein-protein interaction.

XX Unidentified.

XX MO200253700-A2.

XX 11-JUL-2002.

XX 31-DEC-2001; 2001WO-US049442.

XX 29-DEC-2000; 2000US-00751181.

XX 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Lazarovits J, Hagai Y, Plaksain D, Vogel T, Nimrod A, Mar-Haim H;

XX Stanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in

XX physiological phenomena such as cell rolling, metastasis and

XX inflammation, for treating autoimmune, inflammatory or cardiovascular

XX diseases, and cancer.

XX PS Disclosure; Fig 52; 0pp; English.

XX The invention relates to an isolated epitope present on cancer cells and

XX important in physiological phenomena such as cell rolling, metastasis and

XX inflammation, where the epitope is capable of being bound by an antibody,

XX its antigen-binding fragment or its complex comprising at least one

XX antibody or its binding fragment having a first hypervariable region. The

XX epitopes are useful for inhibiting cell rolling, inflammation, autoimmune

XX disease, thrombosis, restenosis, metastasis, growth and/or replication of

XX tumour or leukaemia cells, increase in number of tumour or leukaemia

XX cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-

XX platelet and/or cell-platelet adhesion or aggregation, for increasing

XX mortality of tumour or leukaemia cells, for increasing the susceptibility

XX of diseased cells to damage by anti-disease, anti-cancer or anti-

XX leukaemia agents, or for decreasing the number of tumour or leukaemia

XX cells in a patient, or in the manufacture of a medicament for the above

XX mentioned purposes. The epitopes are useful for diagnosing and treating

XX diseases, cardiovascular diseases such as myocardial infarction,

XX retinopathic diseases and other diseases mediated by abnormal platelet

XX function and diseases caused by sulphated tyrosine-dependent protein-

XX protein interactions. This sequence represents an antibody protein of the

XX invention

XX SO Sequence 246 AA;

XX Query Match 100.0%; Score 29; DB 5; Length 246;

XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;

XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 MRAPVI 6

XX Db 100 MRAPVI 105

XX RESULT 8

XX ABG78334

XX ID ABG78334 standard; protein; 256 AA.

XX AC ABG78334;

AC ABG78334;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Human Fv molecule hypervariable region related peptide #209.  
 XX  
 XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;  
 KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukemia; adenoma;  
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200253264-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 31-DEC-2001; 2001WO-US049440.  
 XX  
 PR 29-DEC-2000; 2000US-00751181.  
 XX  
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 XX  
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;  
 PI Plakain D, Peretz T;  
 XX  
 DR WPI; 2002-619166/66.  
 XX  
 PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 PT or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favor of other  
 PT cells.  
 XX  
 PS Example 9; Page 90; 232pp; English.  
 XX  
 CC The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention  
 CC  
 XX  
 SQ Sequence 256 AA;  
 XX  
 QY  
 DB 100 MRAPVI 105

Query Match 100.0%; Score 29; DB 5; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRAPVI 6  

RESULT 9  
 ABG92025  
 ID ABG92025 standard; protein; 256 AA.  
 XX  
 AC ABG92025;  
 XX  
 DT 04-DEC-2002 (first entry)  
 XX  
 DE Antibody biotag #1.  
 XX  
 KM Antibody; antibody biotag; cancer; tumour; cell rolling; inflammation;  
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;

KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
 KM myocardial infarction; retinopathic disease; abnormal platelet function;  
 KM sulphated tyrosine-dependent protein-protein interaction.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200253700-A2.  
 XX  
 PD 11-JUL-2002.  
 XX  
 PF 31-DEC-2001; 2001WO-US049442.  
 XX  
 PR 29-DEC-2000; 2000US-00751181.  
 PR 29-DEC-2000; 2000US-0258948P.  
 XX  
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 XX  
 PI Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;  
 PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;  
 XX  
 DR WPI; 2002-674776/72.  
 XX  
 PS Disclosure; Fig 51; 0pp; English.  
 XX  
 CC The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
 CC tumour or leukemia cells, increase in number of tumour or leukemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
 CC mortality of tumour or leukemia cells, for increasing the susceptibility  
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
 CC leukemia agents, or for decreasing the number of tumour or leukemia  
 CC cells in a patient, or in the manufacture of a medicament for the above  
 CC mentioned purposes. The epitopes are useful for diagnosing and treating  
 CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory  
 CC diseases, cardiovascular diseases such as myocardial infarction,  
 CC retinopathic diseases and other diseases mediated by abnormal platelet  
 CC function and diseases caused by sulphated tyrosine-dependent protein-  
 CC protein interactions. This sequence represents an antibody biotag used in  
 CC the scope of the invention  
 CC  
 XX  
 SQ Sequence 256 AA;  
 XX  
 QY  
 DB 100 MRAPVI 105

Query Match 100.0%; Score 29; DB 5; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRAPVI 6  

RESULT 10  
 ABG92020  
 ID ABG92020 standard; protein; 266 AA.  
 XX  
 AC ABG92020;  
 XX  
 DT 04-DEC-2002 (first entry)  
 XX  
 DE Human antibody fragment #204.  
 XX  
 KM Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;

KW metastasis; hypervariable region; autoimmune disease; thrombosis;  
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
 KW myocardial infarction; retinopathic disease; abnormal platelet function;  
 KW sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.

PN WO200253700-A2.

XX 11-JUL-2002.

XX 31-DEC-2001; 2001WO-US049442.

XX 29-DEC-2000; 2000US-00751181.

PR 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
 PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX MPI; 2002-674776/72.

PT Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer.

PS Disclosure; Page 309-310; Opp; English.

CC The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility  
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
 CC leukemia agents, or for decreasing the number of tumour or leukaemia  
 CC cells in a patient, or in the manufacture of a medicament for the above  
 CC mentioned purposes. The epitopes are useful for diagnosing and treating  
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
 CC diseases, cardiovascular diseases such as myocardial infarction,  
 CC retinopathic diseases and other diseases mediated by abnormal platelet  
 CC function and diseases caused by sulphated tyrosine-dependent protein-  
 CC protein interactions. This sequence represents a human antibody fragment  
 CC of the invention

SO Sequence 266 AA;

Query Match 100.0%; Score 29; DB 5; Length 266;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6

DB 121 MRAPI 126

RESULT 11

ABG78150

XX ABG78150 standard; protein; 277 AA.

DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #25.

KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;  
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

OS Homo sapiens.

PN WO200259264-A2.

XX 01-AUG-2002.

XX 31-DEC-2001; 2001WO-US049440.

XX 29-DEC-2000; 2000US-00751181.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;  
 PI Plaksin D, Peretz T;

XX MPI; 2002-619166/66.

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 PT or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favor of other  
 PT cells.

PS Claim 4; Page 155-156; 232pp; English.

CC The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention

SO Sequence 277 AA;

Query Match 100.0%; Score 29; DB 5; Length 277;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6

DB 121 MRAPI 126

RESULT 12

ABG91841

XX ABG91841 standard; protein; 277 AA.

DT 04-DEC-2002 (first entry)

DE Human antibody fragment #25.

KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;  
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
 KW myocardial infarction; retinopathic disease; abnormal platelet function;  
 KW sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.

PF	XX	30-JUN-2003; 2003WO-US020604.
XX	XX	
PR	XX	01-JUL-2002; 2002US-00189025.
XX	XX	
PA	XX	(SAVI-) SAVIENT PHARM INC.
PI	XX	Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
DR	XX	WPI; 2004-099189/10.
PT	XX	Composition comprising an agent and/or antibody or its fragment, useful
PT	XX	for treating auto-immune disease, thrombosis, restenosis, metastasis, or
PT	XX	for inhibiting growth and/or replication of tumor cells or leukemia
PT	XX	cells.
PS	XX	Claim 13; SEQ ID NO 1; 58pp; English.
CC	XX	
CC	XX	The present sequence is the protein sequence of human scFv fragment Y1.
CC	XX	This antibody was identified by screening a human antibody phage library
CC	XX	that has diversity only in the heavy chain CDS regions. Fixed human
CC	XX	platelets were screened in order to identify antibodies that bind
CC	XX	platelets. The epitope for Y1 antibody is located between amino acids 272
CC	XX	and 285 on glycoalbumin, a subunit of the CD42 complex. Y1 also binds the
CC	XX	N-terminal of PSGL-1, a receptor for E-, L- and P-selectins, and has a
CC	XX	high affinity for primary leukaemia cells. The invention relates to
CC	XX	compositions utilising an agent and an antibody or its fragment. The
CC	XX	agent is a toxin, radioisotope or pharmaceutical agent such as
CC	XX	doxorubicin. It is complexed or combined with or conjugated to the
CC	XX	antibody or its fragment. The agent and/or antibody can be present in the
CC	XX	composition is a sub-clinical amount, i.e. less than the amount generally
CC	XX	found to be clinically effective when the agent is administered alone.
CC	XX	The composition is used in claimed methods of: inhibiting cell rolling,
CC	XX	inflammation, thrombosis, restenosis, metastasis, the growth and/or
CC	XX	replication of tumour cells or leukemia cells, an increase in number of
CC	XX	tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,
CC	XX	platelet-platelet and/or cell-platelet complex formation, aggregation or
CC	XX	adhesion; increasing the mortality rate of tumour or leukemia cells, the
CC	XX	susceptibility of disease cells to damage by anti-disease agents, and the
CC	XX	susceptibility of tumour or leukemia cells to damage by anti-cancer
CC	XX	agents; and ameliorating the effects of a disease, preventing a disease,
CC	XX	treating a disease or inhibiting the progress of a disease.
XX	XX	
SQ	XX	Sequence 277 AA;
QY	1 MRAPV1 6       	100.0%; Score 29; DB 8; Length 277; Best Local Similarity 100.0%; Pred. No. 1.7e+2; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Db	121 MRAPV1 126	
RESULT 14		
ID	AD128367	standard; protein; 278 AA.
AC	AD128367;	
DT	06-MAY-2004	(first entry)
DE	Human scFv fragment Y17, binds to platelets.	
KW	Human; antibody; scFv; platelet; drug delivery; cancer; therapy.	
OS	Homo sapiens.	
PX	MO2004002528-A1.	
PN	08-JAN-2004.	
PD	30-JUN-2003; 2003WO-US020604.	
XP		

XX 01-JUL-2002; 2002US-00189025.  
 PR (SAVI-) SAVIENT PHARM INC.  
 XX PA Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;  
 XX PI MPI; 2004-099189/10.  
 DR  
 XX Composition comprising an agent and/or antibody or its fragment, useful  
 PT for treating auto-immune disease, thrombosis, restenosis, metastasis, or  
 PT for inhibiting growth and/or replication of tumor cells or leukemia  
 cells.  
 PS Claim 13; SEQ ID NO 2; 58pp; English.  
 XX  
 CC The present sequence is the protein sequence of human scFv fragment Y17.  
 CC This antibody was identified by screening a human antibody phage library  
 CC that has diversity only in the heavy chain CDR3 regions. Fixed human  
 CC platelets were screened in order to identify antibodies that bind  
 CC platelets. Y17 binds leukemic cells. The invention relates to  
 CC compositions utilising an agent and an antibody or its fragment. The  
 CC agent is a toxin, radioisotope or pharmaceutical agent such as  
 CC doxorubicin. It is complexed or combined with or conjugated to the  
 CC antibody or its fragment. The agent and/or antibody can be present in the  
 CC composition as a sub-clinical amount, i.e. less than the amount generally  
 CC found to be clinically effective when the agent is administered alone.  
 CC The composition is used in claimed methods of: inhibiting cell rolling,  
 CC inflammation, thrombosis, restenosis, metastasis, the growth and/or  
 CC replication of tumour cells or leukaemia cells, an increase in number of  
 CC tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,  
 CC platelet-platelet and/or cell-platelet complex formation, aggregation or  
 CC adhesion; increasing the mortality rate of tumour or leukaemia cells, the  
 CC susceptibility of disease cells to damage by anti-disease agents, and the  
 CC susceptibility of tumour or leukaemia cells to damage by anti-cancer  
 CC agents; and ameliorating the effects of a disease, preventing a disease,  
 CC treating a disease or inhibiting the progress of a disease.  
 CC  
 SQ Sequence 278 AA;  
 XX  
 Query Match 100.0%; Score 29; DB 8; Length 278;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY - 1 MRAPVI 6  
 Db 122 MRAPVI 127  
 XX  
 RESULT 15  
 ADI28368  
 ID ADI28368 standard; protein; 280 AA.  
 AC ADI28368;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Human scFv fragment L32, binds to leukaemia cells.  
 XX  
 KM Human; antibody; scFv; leukaemia; drug delivery; cancer; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004002528-A1.  
 PD  
 XX 08-JAN-2004.  
 XX  
 PF 30-JUN-2003; 2003WO-US020604.  
 XX  
 PR 01-JUL-2002; 2002US-00189025.  
 XX  
 PA (SAVI-) SAVIENT PHARM INC.  
 XX

PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;  
 XX MPI; 2004-099189/10.  
 DR  
 XX Composition comprising an agent and/or antibody or its fragment, useful  
 PT for treating auto-immune disease, thrombosis, restenosis, metastasis, or  
 PT for inhibiting growth and/or replication of tumor cells or leukemia  
 cells.  
 PS Claim 13; SEQ ID NO 3; 58pp; English.  
 XX  
 CC The present sequence is the protein sequence of human scFv fragment L32.  
 CC This antibody was identified by screening a human antibody phage library  
 CC that has diversity only in the heavy chain CDR3 regions. Leukaemia cells  
 CC were screened to select specific antibodies that recognise leukaemia cell  
 CC surface determinants. The invention relates to compositions utilising an  
 CC agent and an antibody or its fragment. The agent is a toxin, radioisotope  
 CC or pharmaceutical agent such as doxorubicin. It is complexed or combined  
 CC with or conjugated to the antibody or its fragment. The agent and/or  
 CC antibody can be present in the composition as a sub-clinical amount, i.e.  
 CC less than the amount generally found to be clinically effective when the  
 CC agent is administered alone. The composition is used in claimed methods  
 CC of: inhibiting cell rolling, inflammation, thrombosis, restenosis,  
 CC metastasis, the growth and/or replication of tumour cells or leukaemia  
 CC cells, an increase in number of tumour or leukaemia cells, cell-cell,  
 CC cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet  
 CC complex formation, aggregation or adhesion; increasing the mortality rate  
 CC of tumour or leukaemia cells, the susceptibility of disease cells to  
 CC damage by anti-disease agents, and the susceptibility of tumour or  
 CC leukaemia cells to damage by anti-cancer agents; and ameliorating the  
 CC effects of a disease, preventing a disease, treating a disease or  
 CC inhibiting the progress of a disease.  
 CC  
 SQ Sequence 280 AA;  
 XX  
 Query Match 100.0%; Score 29; DB 8; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRAPVI 6  
 Db 124 MRAPVI 129  
 XX  
 Search completed: April 25, 2005, 20:22:22  
 Job time : 8.67849 secs

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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:24:31 ; Search time 0.924612 Seconds  
(without alignments)  
484.413 Million cell updates/sec

Title: US-10-029-926D-8

Perfect score: 29

Sequence: 1 MRAPVI 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A COMB pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B COMB pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A COMB pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B COMB pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTCUS COMB pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pdp:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	96.6	973	4 US-09-252-991A-23944	Sequence 23944, A
2	26	89.7	229	4 US-09-248-796A-16460	Sequence 16460, A
3	26	89.7	286	4 US-09-711-164-385	Sequence 385, App
4	26	89.7	350	4 US-09-198-452A-643	Sequence 643, App
5	26	89.7	350	4 US-09-438-185A-605	Sequence 605, App
6	26	89.7	477	4 US-09-489-039A-8906	Sequence 8906, App
7	25	86.2	119	4 US-09-252-991A-28425	Sequence 28425, A
8	25	86.2	130	4 US-09-107-532A-6688	Sequence 6688, A
9	25	86.2	197	4 US-09-902-540-13013	Sequence 13013, A
10	25	86.2	222	4 US-09-489-039A-8244	Sequence 8244, App
11	25	86.2	222	4 US-09-538-092-272	Sequence 272, App
12	25	86.2	223	4 US-09-134-000C-6010	Sequence 6010, App
13	25	86.2	224	4 US-09-538-092-617	Sequence 617, App
14	25	86.2	233	4 US-09-489-039A-7366	Sequence 7366, App
15	25	86.2	239	4 US-09-328-352-5866	Sequence 5866, App
16	25	86.2	291	4 US-09-602-777A-36	Sequence 36, App1
17	25	86.2	359	4 US-09-252-991A-19964	Sequence 19964, A
18	25	86.2	417	4 US-09-270-767-4567	Sequence 4567, A
19	25	86.2	481	4 US-09-252-991A-26783	Sequence 26783, A
20	25	86.2	481	4 US-09-489-039A-10515	Sequence 10515, A
21	25	86.2	487	4 US-09-583-110-3569	Sequence 3569, App
22	25	86.2	488	4 US-09-107-433-3552	Sequence 3552, App
23	25	86.2	657	4 US-09-252-991A-27682	Sequence 27682, App
24	25	86.2	885	4 US-09-902-540-13431	Sequence 13431, A
25	25	86.2	962	4 US-09-328-352-7942	Sequence 7942, App
26	24	82.8	73	4 US-09-621-976-6392	Sequence 6392, App
27	24	82.8	76	4 US-09-636-215-575	Sequence 575, App

28	24	82.8	76	4 US-09-685-166A-575	Sequence 575, App
29	24	82.8	76	4 US-09-685-166A-888	Sequence 888, App
30	24	82.8	76	4 US-09-679-426-575	Sequence 575, App
31	24	82.8	76	4 US-09-679-426-888	Sequence 888, App
32	24	82.8	76	4 US-09-759-143-575	Sequence 575, App
33	24	82.8	76	4 US-09-759-143-888	Sequence 888, App
34	24	82.8	76	4 US-09-651-736-575	Sequence 575, App
35	24	82.8	82	3 US-09-134-001C-4676	Sequence 4676, App
36	24	82.8	89	3 US-09-134-001C-4563	Sequence 4563, App
37	24	82.8	93	4 US-09-938-806A-8	Sequence 8, App1
38	24	82.8	102	4 US-09-248-796A-14433	Sequence 14433, A
39	24	82.8	108	4 US-09-513-999C-5944	Sequence 5944, App
40	24	82.8	125	3 US-09-199-637A-403	Sequence 403, App
41	24	82.8	125	4 US-09-269-410-11	Sequence 11, App1
42	24	82.8	125	4 US-09-513-999C-5838	Sequence 5838, App
43	24	82.8	143	4 US-09-270-767-42631	Sequence 42631, A
44	24	82.8	162	3 US-08-801-742-3	Sequence 3, App1
45	24	82.8	192	1 US-08-208-008C-9	Sequence 9, App1

## ALIGNMENTS

```
RESULT 1
US-09-252-991A-23944
; Sequence 23944, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074.788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094.190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23944
; LENGTH: 973
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23944

Query Match      96.6% Score 28; DB 4; Length 973;
Best Local Similarity 83.3% Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy      1 MRAPVI 6
Db      387 MRAPV 392

RESULT 2
US-09-248-796A-16460
; Sequence 16460, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074.725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096.409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16460
; LENGTH: 229
; TYPE: PRT
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ORGANISM: Candida albicans  
US-09-248-796A-16460

Query Match  
Best Local Similarity 89.7%; Score 26; DB 4; Length 229;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6  
Db 182 MKAPI 187

RESULT 3  
US-09-711-164-385

; Sequence 385, Application US/09711164  
; Patent No. 6589738  
; GENERAL INFORMATION:  
; APPLICANT: Forsyth, R. Allyn  
; APPLICANT: Olsen, Karl  
; APPLICANT: Zyskind, Judith  
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERAPY  
; FILE REFERENCE: ELITRA.008A  
; CURRENT APPLICATION NUMBER: US/09/711.164  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: US 60/164415  
; NUMBER OF SEQ ID NOS: 469  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 385  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-09-711-164-385

Query Match  
Best Local Similarity 89.7%; Score 26; DB 4; Length 286;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6  
Db 41 MRSPVI 46

RESULT 4

US-09-198-452A-643  
; Sequence 643, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198.452A  
; PRIOR FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 643  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-643

Query Match  
Best Local Similarity 89.7%; Score 26; DB 4; Length 350;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6  
Db 109 LRAPVI 114

RESULT 5  
US-09-438-185A-605

; Sequence 605, Application US/09438185A  
; Patent No. 6822071  
; GENERAL INFORMATION:  
; APPLICANT: Stephens, Richard  
; APPLICANT: Mitchell, Wayne  
; APPLICANT: Kalman, Sue  
; APPLICANT: Davis, Ronald  
; TITLE OF INVENTION: The Regents of the University of California  
; FILE REFERENCE: 018941-000411US  
; CURRENT APPLICATION NUMBER: US/09/438.185A  
; PRIOR FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/108.279  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/128.606  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 1074  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 605  
; LENGTH: 350  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; OTHER INFORMATION: Cpn0603  
US-09-438-185A-605

Query Match  
Best Local Similarity 89.7%; Score 26; DB 4; Length 350;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6  
Db 109 LRAPVI 114

RESULT 6  
US-09-489-039A-8906

; Sequence 8906, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489.039A  
; PRIOR FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117.747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 8906  
; LENGTH: 477  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-8906

Query Match  
Best Local Similarity 89.7%; Score 26; DB 4; Length 477;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6  
Db 269 MKAPI 274

RESULT 7  
US-09-252-991A-28425

; Sequence 28425, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136



;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; CURRENT FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO 28425  
;; LENGTH: 119  
;; TYPE: PRT  
;; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-28425

Query Match 86.2%; Score 25; DB 4; Length 119;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
Db 63 MRAPTI 68

RESULT 8  
US-09-107-532A-6688  
; Sequence 6688, Application US/09107532A  
; Patent No. 6583275

;; GENERAL INFORMATION:

;; APPLICANT: Lynn A Doucette-Stamm and David Bush

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
;; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

;; NUMBER OF SEQUENCES: 7310

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

;; STREET: 100 Beaver Street

;; CITY: Waltham

;; STATE: Massachusetts

;; COUNTRY: USA

;; ZIP: 02354

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: CD-ROM ISO9660

;; COMPUTER: PC

;; OPERATING SYSTEM: <Unknown>

;; SOFTWARE: ASCII

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/107,532A

;; FILING DATE: 30-Jun-1998

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 60/085,598

;; FILING DATE: 14 May 1998

;; APPLICATION NUMBER: 60/051571

;; FILING DATE: July 2, 1997

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Arinello, Pamela Deneka

;; REGISTRATION NUMBER: 40,489

;; REFERENCE/DOCKET NUMBER: GTC-012

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (781)893-5007

;; TELEFAX: (781)893-8277

;; INFORMATION FOR SEQ ID NO: 6688:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 120 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; HYPOTHETICAL: YES

;; ORIGINAL SOURCE:

;; ORGANISM: Enterococcus faecium

;; FEATURE:

;; NAME/KEY: misc feature

;; LOCATION: (B) LOCATION 1...120

;; SEQUENCE DESCRIPTION: SEQ ID NO: 6688:

US-09-107-532A-6688

Query Match 86.2%; Score 25; DB 4; Length 120;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
Db 17 MKAPTI 22

RESULT 9  
US-09-902-540-13013  
; Sequence 13013, Application US/09902540  
; Patent No. 6833447

;; GENERAL INFORMATION:

;; APPLICANT: Goldman, Barry S.

;; APPLICANT: Hinkle, Gregory J.

;; APPLICANT: Slater, Steven C.

;; APPLICANT: Wiegand, Roger C.

;; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

;; FILE REFERENCE: 38-10(15849)B

;; CURRENT APPLICATION NUMBER: US/09/902,540

;; FILING DATE: 2001-07-10

;; PRIOR APPLICATION NUMBER: 60/217,883

;; PRIOR FILING DATE: 2000-07-10

;; NUMBER OF SEQ ID NOS: 16825

;; SEQ ID NO 13013

;; LENGTH: 197

;; TYPE: PRT

;; ORGANISM: Myxococcus xanthus

US-09-902-540-13013

Query Match 86.2%; Score 25; DB 4; Length 197;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 5  
Db 1 MRAPV 5

RESULT 10  
US-09-489-039A-8244  
; Sequence 8244, Application US/09489039A  
; Patent No. 6610836

;; GENERAL INFORMATION:

;; APPLICANT: Gary Breton et. al

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

;; FILE REFERENCE: 2709.2004001

;; CURRENT APPLICATION NUMBER: US/09/489,039A

;; FILING DATE: 2000-01-27

;; PRIOR APPLICATION NUMBER: US 60/117,747

;; PRIOR FILING DATE: 1999-01-29

;; NUMBER OF SEQ ID NOS: 14342

;; SEQ ID NO 8244

;; LENGTH: 222

;; TYPE: PRT

;; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-8244

Query Match 86.2%; Score 25; DB 4; Length 222;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 5  
Db 24 MRAPV 28

RESULT 11  
US-09-538-092-272  
; Sequence 272, Application US/09538092  
; Patent No. 6753314

GENERAL INFORMATION:  
APPLICANT: Glot, Loic  
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
FILE REFERENCE: 15966-542  
CURRENT APPLICATION NUMBER: US/09/538,092  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: 60/127,352  
PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: 60/178,965  
PRIOR FILING DATE: 2000-02-01  
NUMBER OF SEQ ID NOS: 1387  
SOFTWARE: CuraPatSeqFormatVer Version 0.9  
SEQ ID NO 272  
LENGTH: 222  
TYPE: PRT  
ORGANISM: Saccharomyces cerevisiae  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (0)...(0)  
OTHER INFORMATION: Polypeptide Accession Number YFL060C  
US-09-538-092-272

Query Match 86.2%; Score 25; DB 4; Length 222;  
Best Local Similarity 83.3%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 6  
:|||||  
Db 151 IRAPV 156

RESULT 12  
US-09-134-000C-6010  
Sequence 6010, Application US/09134000C  
Patent No. 6617156  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 032796-032  
CURRENT APPLICATION NUMBER: US/09/134,000C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/055,778  
PRIOR FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 6812  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6010  
LENGTH: 223  
TYPE: PRT  
ORGANISM: Enterococcus faecalis  
US-09-134-000C-6010

Query Match 86.2%; Score 25; DB 4; Length 223;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 5  
:|||||  
Db 127 MRAPV 131

RESULT 13  
US-09-538-092-617  
Sequence 617, Application US/09538092  
Patent No. 6753314  
GENERAL INFORMATION:  
APPLICANT: Glot, Loic  
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
FILE REFERENCE: 15966-542  
CURRENT APPLICATION NUMBER: US/09/538,092  
CURRENT FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 60/127,352  
PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: 60/178,965  
PRIOR FILING DATE: 2000-02-01  
NUMBER OF SEQ ID NOS: 1387  
SOFTWARE: CuraPatSeqFormatVer Version 0.9  
SEQ ID NO 617  
LENGTH: 224  
TYPE: PRT  
ORGANISM: Saccharomyces cerevisiae  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (0)...(0)  
OTHER INFORMATION: Polypeptide Accession Number YMR095C  
US-09-538-092-617

Query Match 86.2%; Score 25; DB 4; Length 224;  
Best Local Similarity 83.3%; Pred. No. 4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 6  
:|||||  
Db 160 IRAPV 165

RESULT 14  
US-09-489-039A-7366  
Sequence 7366, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 7366  
LENGTH: 233  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-7366

Query Match 86.2%; Score 25; DB 4; Length 233;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 5  
:|||||  
Db 173 MRAPV 177

RESULT 15  
US-09-328-352-5866  
Sequence 5866, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 5866  
LENGTH: 239  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-5866

Query Match 86.2%; Score 25; DB 4; Length 239;

Best Local Similarity 66.7%; Pred. No. 4.3e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6  
|:|:|:  
Db 140 MKAPVV 145

Search completed: April 25, 2005, 21:12:11  
Job time : 1.92461 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:22:46 ; Search time 2.6541 Seconds  
(without alignments)  
752.325 Million cell updates/sec

Title: US-10-029-926D-8

Perfect score: 29

Sequence: 1 MRAPIV 6

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

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2: /cgn2\_6/ptodata/2/pubppa/PCRT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubppa/PCRTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep:\*

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10: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubppa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubppa/US09C\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*

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16: /cgn2\_6/ptodata/2/pubppa/US10C\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/2/pubppa/US10C\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubppa/US10C\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	15	US-10-032-037B-8
2	29	100.0	6	15	US-10-029-988B-8
3	29	100.0	6	15	US-10-032-423A-8
4	29	100.0	6	15	US-10-029-926B-8
5	29	100.0	6	17	US-10-880-922-4
6	29	100.0	266	15	US-10-032-037B-204
7	29	100.0	266	15	US-10-029-988B-204
8	29	100.0	266	15	US-10-032-423A-204
9	29	100.0	277	15	US-10-032-037B-25
10	29	100.0	277	15	US-10-029-988B-25
11	29	100.0	277	15	US-10-032-423A-25
12	29	100.0	277	15	US-10-029-926B-25
13	29	100.0	442	15	US-10-369-493-7871

14	29	100.0	464	15	US-10-032-037B-26	Sequence 26, Appl
15	29	100.0	464	15	US-10-029-988B-26	Sequence 26, Appl
16	29	100.0	464	15	US-10-032-423A-26	Sequence 26, Appl
17	29	100.0	464	15	US-10-029-926B-26	Sequence 26, Appl
18	29	96.6	86	15	US-10-424-599-253048	Sequence 253048,
19	29	96.6	123	15	US-10-424-599-150638	Sequence 150638,
20	29	96.6	438	9	US-09-908-419-2	Sequence 2, Appl
21	29	96.6	438	14	US-10-056-790-2	Sequence 2, Appl
22	29	96.6	438	14	US-10-056-790-36	Sequence 36, Appl
23	29	96.6	438	14	US-10-056-790-46	Sequence 46, Appl
24	29	96.6	511	9	US-09-738-626-3996	Sequence 3996, Ap
25	29	93.1	99	15	US-10-424-599-272558	Sequence 272558,
26	29	89.7	112	15	US-10-767-701-42410	Sequence 42410, A
27	29	89.7	226	14	US-10-032-585-7418	Sequence 7418, Ap
28	29	89.7	286	14	US-10-287-274-385	Sequence 385, Ap
29	29	89.7	286	15	US-10-369-493-23563	Sequence 23563, A
30	29	89.7	286	15	US-10-282-122A-43216	Sequence 43216, A
31	29	89.7	289	15	US-10-425-114-69148	Sequence 69148, A
32	29	89.7	290	15	US-10-282-122A-56193	Sequence 56193, A
33	29	89.7	319	15	US-10-425-114-55531	Sequence 55531, A
34	29	89.7	345	16	US-10-767-701-45307	Sequence 45307, A
35	29	89.7	350	15	US-10-289-762-643	Sequence 643, Ap
36	29	89.7	405	14	US-10-017-161-2090	Sequence 2090, Ap
37	29	89.7	405	15	US-10-292-795-1336	Sequence 1736, Ap
38	29	89.7	514	15	US-10-425-114-53835	Sequence 53835, A
39	29	89.7	530	15	US-10-425-114-60637	Sequence 60637, A
40	29	89.7	530	16	US-10-437-963-144989	Sequence 144989,
41	29	86.2	58	16	US-10-437-963-117085	Sequence 137085,
42	29	86.2	73	15	US-10-767-701-48548	Sequence 48548, A
43	29	86.2	63	15	US-10-424-599-196866	Sequence 196866,
44	29	86.2	104	16	US-10-437-963-164399	Sequence 164399,
45	29	86.2	110	16	US-10-437-963-158848	Sequence 158848,

#### ALIGNMENTS

RESULT 1  
US-10-032-037B-8  
; Sequence 8, Application US/10032037B  
; Publication No. US20040001822A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/44  
; CURRENT APPLICATION NUMBER: US/10/032,037B  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-037B-8

Query Match 100.0%; Score 29; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPIV 6  
|||||  
Db 1 MRAPIV 6

RESULT 2  
US-10-029-988B-8  
; Sequence 8, Application US/10029988B  
; Publication No. US20040001839A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.

;; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
;; FILE REFERENCE: 10793/46  
;; CURRENT APPLICATION NUMBER: US/10/029, 988B  
;; PRIOR FILING DATE: 2001-12-31  
;; PRIOR APPLICATION NUMBER: 60/258,948  
;; NUMBER OF SEQ ID NOS: 204  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 8  
;; LENGTH: 6  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-029-988B-8

Query Match 100.0%; Score 29; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
| | | | |  
Db 1 MRAPVI 6

RESULT 3  
US-10-032-423A-8  
; Sequence 8, Application US/10032423A  
; Publication No. US20040002450A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/45  
; CURRENT APPLICATION NUMBER: US/10/032,423A  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 12/29/2000  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-423A-8

Query Match 100.0%; Score 29; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
| | | | |  
Db 1 MRAPVI 6

RESULT 4  
US-10-029-926B-8  
; Sequence 8, Application US/10029926B  
; Publication No. US20040073011A1  
; GENERAL INFORMATION:  
; APPLICANT: HAGAY, et al.  
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY  
; FILE REFERENCE: 10793/50  
; CURRENT APPLICATION NUMBER: US/10/029,926B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 12/29/2000  
; NUMBER OF SEQ ID NOS: 203  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-029-926B-8

Query Match 100.0%; Score 29; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
| | | | |  
Db 1 MRAPVI 6

RESULT 5  
US-10-880-922-4  
; Sequence 4, Application US/10880922  
; Publication No. US2005006955A1  
; GENERAL INFORMATION:  
; APPLICANT: PLAKSIN, DANIEL  
; APPLICANT: LEVANNON, DANIEL  
; APPLICANT: SZANTON, ESTHER  
; APPLICANT: HAGAY, YOCHAVED  
; APPLICANT: BEN-LEVY, RACHEL  
; APPLICANT: NISGAV, YAEEL  
; APPLICANT: KANFL, YARIV  
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: 10793-143  
; CURRENT APPLICATION NUMBER: US/10/880,922  
; CURRENT FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 60/484,061  
; PRIOR FILING DATE: 2003-06-30  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 4  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-880-922-4

Query Match 100.0%; Score 29; DB 17; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
| | | | |  
Db 1 MRAPVI 6

RESULT 6  
US-10-032-037B-204  
; Sequence 204, Application US/10032037B  
; Publication No. US20040001822A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/44  
; CURRENT APPLICATION NUMBER: US/10/032,037B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 204  
; LENGTH: 266  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-037B-204

Query Match 100.0%; Score 29; DB 15; Length 266;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6  
| | | | |  
Db 121 MRAPI 126

## RESULT 7

US-10-029-988B-204  
; Sequence 204, Application US/10029988B  
; Publication No. US20040001839A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SUFATED  
; FILE REFERENCE: 10793/46  
; CURRENT APPLICATION NUMBER: US/10/029,988B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 204  
; LENGTH: 266  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-029-988B-204

Query Match 100.0%; Score 29; DB 15; Length 266;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6  
| | | | |  
Db 121 MRAPI 126

## RESULT 8

US-10-032-423A-204  
; Sequence 204, Application US/10032423A  
; Publication No. US20040002450A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SUFATED  
; FILE REFERENCE: 10793/45  
; CURRENT APPLICATION NUMBER: US/10/032,423A  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 12/29/2000  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 204  
; LENGTH: 266  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-423A-204

Query Match 100.0%; Score 29; DB 15; Length 266;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6  
| | | | |  
Db 121 MRAPI 126

## RESULT 9

US-10-032-037B-25  
; Sequence 25, Application US/10032037B  
; Publication No. US20040001822A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SUFATED  
; FILE REFERENCE: 10793/44  
; CURRENT APPLICATION NUMBER: US/10/032,037B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-037B-25

FILE REFERENCE: 10793/44  
; CURRENT APPLICATION NUMBER: US/10/032,037B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-037B-25

Query Match 100.0%; Score 29; DB 15; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6  
| | | | |  
Db 121 MRAPI 126

## RESULT 10

US-10-029-988B-25  
; Sequence 25, Application US/10029988B  
; Publication No. US20040001839A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SUFATED  
; FILE REFERENCE: 10793/46  
; CURRENT APPLICATION NUMBER: US/10/029,988B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-029-988B-25

Query Match 100.0%; Score 29; DB 15; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6  
| | | | |  
Db 121 MRAPI 126

## RESULT 11

US-10-032-423A-25  
; Sequence 25, Application US/10032423A  
; Publication No. US20040002450A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SUFATED  
; FILE REFERENCE: 10793/45  
; CURRENT APPLICATION NUMBER: US/10/032,423A  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 12/29/2000  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-423A-25

Query Match 100.0%; Score 29; DB 15; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6  
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 Db 121 MRAPI 126

## RESULT 12

US-10-029-926B-25  
 ; Sequence 25; Application US/10029926B  
 ; Publication No. US2004073011A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HAGAY, et al.  
 ; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY  
 ; FILE REFERENCE: 10793/50  
 ; CURRENT APPLICATION NUMBER: US/10/029,926B  
 ; PRIOR FILING DATE: 2001-12-31  
 ; PRIOR APPLICATION NUMBER: 60/258,948  
 ; NUMBER OF SEQ ID NOS: 203  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 25  
 ; LENGTH: 277  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-029-926B-25

Query Match 100.0%; Score 29; DB 15; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6  
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 Db 121 MRAPI 126

## RESULT 13

US-10-369-493-7871  
 ; Sequence 7871; Application US/10369493  
 ; Publication No. US20030233675A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Chen, Xiandeng  
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 ; FILE REFERENCE: 38-10(52052)B  
 ; CURRENT APPLICATION NUMBER: US/10/369,493  
 ; PRIOR FILING DATE: 2003-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/360,039  
 ; NUMBER OF SEQ ID NOS: 47374  
 ; SEQ ID NO 7871  
 ; LENGTH: 442  
 ; TYPE: PRT  
 ; ORGANISM: Rhodobacter sphaeroides  
 US-10-369-493-7871

Query Match 100.0%; Score 29; DB 15; Length 442;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6  
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 Db 77 MRAPI 82

RESULT 14  
 US-10-032-037B-26

; Sequence 26; Application US/10032037B  
 ; Publication No. US20040001822A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bio-Technology General Corp.  
 ; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
 ; MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
 ; FILE REFERENCE: 10793/44  
 ; CURRENT APPLICATION NUMBER: US/10/032,037B  
 ; PRIOR FILING DATE: 2001-12-31  
 ; PRIOR APPLICATION NUMBER: 60/258,948  
 ; NUMBER OF SEQ ID NOS: 204  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 26  
 ; LENGTH: 464  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-032-037B-26

Query Match 100.0%; Score 29; DB 15; Length 464;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6  
 |||||  
 Db 118 MRAPI 123

## RESULT 15

US-10-029-988B-26  
 ; Sequence 26; Application US/10029988B  
 ; Publication No. US20040001839A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bio-Technology General Corp.  
 ; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
 ; MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF  
 ; FILE REFERENCE: 10793/46  
 ; CURRENT APPLICATION NUMBER: US/10/029,988B  
 ; PRIOR FILING DATE: 2001-12-31  
 ; PRIOR APPLICATION NUMBER: 60/258,948  
 ; NUMBER OF SEQ ID NOS: 204  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 26  
 ; LENGTH: 464  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-029-988B-26

Query Match 100.0%; Score 29; DB 15; Length 464;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPI 6  
 |||||  
 Db 118 MRAPI 123

Search completed: April 25, 2005, 21:09:47  
 Job time : 3.6541 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 19:57:16 ; Search time 0.691796 Seconds

(without alignments)  
834.495 Million cell updates/sec

Title: US-10-029-926D-8

Sequence: 1 MRAPVI 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : PIR 79:\*

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	249	2	H87675 hydroxylase, alpha/b
2	29	100.0	442	2	JC4733 Probable H+-transp
3	29	100.0	629	2	T37255 acetylcholinesterase
4	28	96.6	425	2	S33045 hypothetical prote
5	27	93.1	247	2	H69030 coenzyme PQQ synth
6	26	89.7	286	2	A91131 tagatose-1,6-bisph
7	26	89.7	286	2	A85976 tagatose-bisphosph
8	26	89.7	286	2	B65103 ferriochelataase CP0
9	26	89.7	327	2	E72057 ferriochelataase [im
10	26	89.7	450	1	S13730 pmba protein - Esc
11	26	89.7	450	2	AE1056 probable pmba prot
12	26	89.7	450	2	D86121 maturation of anti
13	26	89.7	450	2	D91280 maturation of anti
14	26	89.7	450	2	D91280 maturation of anti
15	25	86.2	138	2	T24916 hypothetical prote
16	25	86.2	147	2	C95907 probable protein 1
17	25	86.2	147	2	C95924 hypothetical prote
18	25	86.2	149	2	C72419 conserved hypotet
19	25	86.2	144	2	A82812 conserved hypotet
20	25	86.2	163	2	A87412 hypothetical prote
21	25	86.2	195	2	F75399 antibiotic resista
22	25	86.2	196	2	G75405 imidazoleglycerol-
23	25	86.2	203	2	C84409 imidazoleglycerol-
24	25	86.2	222	2	S63320 probable membrane
25	25	86.2	222	2	S56195 probable membrane
26	25	86.2	224	2	S55081 hypothetical prote
27	25	86.2	227	2	C53304 transfer protein C
28	25	86.2	240	2	E69004 hypothetical prote
29	25	86.2	252	2	A88508 protein H14A12.4 (

30	25	86.2	261	2	AC3507 hief protein (impo
31	25	86.2	266	2	AC2407 Cryptophan synthas
32	25	86.2	284	2	AF1341 fructose-1,6-bispho
33	25	86.2	284	2	AD1712 fructose-1,6-bispho
34	25	86.2	328	2	G96024 conserved hypotet
35	25	86.2	332	2	C81285 glyceraldehyde 3-P
36	25	86.2	359	2	A10112 fructose-bisphosph
37	25	86.2	362	2	F90200 hypothetical prote
38	25	86.2	398	2	B70752 hypothetical prote
39	25	86.2	422	2	AE3394 lipoprotein releas
40	25	86.2	422	2	B83083 probable two-compo
41	25	86.2	430	2	T16715 hypothetical prote
42	25	86.2	446	2	A84940 pmba protein (impo
43	25	86.2	463	2	AC0977 L-seeryl-tRNAse ac
44	25	86.2	487	2	T27353 hypothetical prote
45	25	86.2	489	2	JC4787 shaw protein - Cal

#### ALIGNMENTS

RESULT 1  
H87675 hydroxylase, alpha/beta hydroxylase fold family [imported] - Caulobacter crescentus  
C/Species: Caulobacter crescentus  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #ext\_change 12-Jul-2004  
C/Accession: H87675  
R/Nerman, W.C.; Feildblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gattim, M.L.; Hatt, D.H.; Kolos, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A/Title: Complete Genome Sequence of Caulobacter crescentus.  
A/Reference number: A87249; NCID:21173698; PMID:11259647  
A/Accession: H87675  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-249 <STO>  
A/Cross-references: UNIPROT:Q9A2M4; GB:AE005673; NCID:g13425158; PIDD:AAK25404.1; GSPDB:  
C/Genetics:  
A/Gene: CC3442  
C/Superfamily: tropinesterase

Query Match Best Local Similarity 100.0%; Score 29; DB 2; Length 249;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
|||||  
Db 1 MRAPVI 6

RESULT 2  
JC4733 probable H+-transporting two-sector ATPase (EC 3.6.3.14), flagellum-specific - Rhodococcus  
C/Species: Rhodococcus sphaeroides  
C/Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #ext\_change 09-Jul-2004  
C/Accession: JC4733  
R/Bellido, T.; Campos, A.; Camarena, L.; Dreyfus, G.  
Gene 170, 69-72, 1996  
A/Title: Flagellar genes from Rhodococcus sphaeroides are homologous to genes of the fl  
A/Reference number: JC4733; NCID:96200857; PMID:8621091  
A/Accession: JC4733  
A/Molecule type: DNA  
A/Residues: 1-442 <BAL>  
A/Cross-references: UNIPROT:Q53093; GB:U31090; NCID:g1518877; PIDD:AA07344.1; PIDD:g1293  
C/Genetics:  
A/Gene: flII  
C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase a  
C/Keywords: ATP; flagellum; hydroxylase; nucleotide binding; P-loop  
F/168-175/Region: nucleotide-binding motif A (P-loop)  
F/191-207/Region: H+-transporting ATP synthase alpha chain homology <ATP>  
F/242-258/Domain: beta chain #status predicted <BET>

Query Match 100.0%; Score 29; DB 2; Length 442;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
|||||  
DB 77 MRAPVI 82

## RESULT 3

T37255  
acetylcholinesterase (EC 3.1.1.7) 2 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C/Accession: T37255  
R/Graus, M.; Chiletto, E.; Combes, D.; Fedon, Y.; Toulant, J.P.; Arpagau, M.  
FEBS Lett. 424, 279-284, 1998  
A/Title: Existence of four acetylcholinesterase genes in the nematode Caenorhabditis el  
A/Reference number: Z21648; MUID:98198570; PMID:9539167  
A/Accession: T37255  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: mRNA  
A/Residues: 1-629 <GRA>  
A/Cross-references: UNIPROT:O61371; EMBL:AF025378; NID:95148937; PIDN:AA14016.2; PID:95  
A/Experimental source: strain N2  
C/Genetics:  
A/Gene: ace-2  
A/Map position: I  
C/Superfamily: cholinesterase; cholinesterase homology  
C/Keywords: carboxylic ester hydrolase

Query Match 100.0%; Score 29; DB 2; Length 629;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
|||||  
DB 1 MRAPVI 6

## RESULT 4

S33045  
hypothetical protein - human herpesvirus 4  
C/Species: human herpesvirus 4, Epstein-Barr virus  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S33045  
R/Farrell, P.J.  
submitted to the EMBL Data Library, March 1988  
A/Reference number: S32973  
A/Accession: S33045  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-425 <FAR>  
A/Cross-references: UNIPROT:P30119; EMBL:V01555; NID:959074; PIDN:CAA24796.1; PID:913349  
C/Superfamily: equine herpesvirus 2 hypothetical protein 23

Query Match 96.6%; Score 28; DB 2; Length 425;  
Best Local Similarity 83.3%; Pred. No. 42;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
|||||  
DB 87 MRAPVI 92

## RESULT 5

H69030  
coenzyme PQQ synthesis protein III - Methanobacterium thermoautotrophicum (strain Delta  
C/Species: Methanobacterium thermoautotrophicum  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: H69030  
R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N  
ki, S.; Church, G.M.; Daniele, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct  
A/Reference number: A69000; MUID:98037514; PMID:9371463  
A/Accession: H69030  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-247 <MTH>  
A/Cross-references: UNIPROT:Q27295; GB:AE000890; GB:AE000666; NID:92622311; PIDN:AA8571  
A/Experimental source: strain Delta H

C/Genetics:

A/Gene: MTH127

A/Start codon: GTG

C/Keywords: iron; metalloprotein

F/34,38,41/Binding site: iron (Cys) #status predicted

Query Match 93.1%; Score 27; DB 2; Length 247;  
Best Local Similarity 66.7%; Pred. No. 42;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
|||||  
DB 4 MRAPVI 9

## RESULT 6

A91131  
tagatose-1,6-bisphosphate aldolase [imported] - Escherichia coli (strain O157:H7, substra  
C/Species: Escherichia coli  
C/Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C/Accession: A91131  
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shibata, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
A/Reference number: A99629; MUID:21156231; PMID:11258796  
A/Accession: A91131  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-266 <HAY>  
A/Cross-references: UNIPROT:P42908; GB:BA000007; PIDN:BA837440.1; PID:913363490; GSPDB:  
A/Experimental source: strain O157:H7, substrain RIMD 0509952  
C/Genetics:  
A/Gene: ECA4017  
C/Superfamily: fructose-bisphosphate aldolase II

Query Match 89.7%; Score 26; DB 2; Length 286;  
Best Local Similarity 83.3%; Pred. No. 89;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
|||||  
DB 41 MRAPVI 46

## RESULT 7

A85976  
tagatose-bisphosphate aldolase 2 [imported] - Escherichia coli (strain O157:H7, substra  
C/Species: Escherichia coli  
C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: A85976  
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca  
Nature 409, 529-533, 2001  
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A/Reference number: A85480; MUID:21074935; PMID:11206551  
A/Accession: A85976  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1286 <STO>  
A/Cross-references: UNIPROT:P42908; GB:AE005174; NID:912517735; PIDN:AA58269.1; GSPDB:  
A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:  
A/Genes: agay  
C/Superfamily: fructose-bisphosphate aldolase II

Query Match 89.7%; Score 26; DB 2; Length 286;  
Best Local Similarity 83.3%; Pred. No. 89;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
DB 41 MRSPVI 46

## RESULT 8

B65103  
ferrochelatase aldolase agay (EC 4.1.2.-) - Escherichia coli (strain K-12)  
C/Species: Escherichia coli  
C/Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C/Accession: B65103  
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A/Title: The complete genome sequence of Escherichia coli K-12.  
A/Reference number: A64720; PMID:9742617; PMID:9278503  
A/Accession: B65103  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-286 <BLAT>  
A/Cross-references: UNIPROT:P42908; GB:AE000395; GB:U00096; NID:G1789524; PIDN:AACT6171.  
A/Experimental source: strain K-12, substrain MG1655  
C/Genetics:  
A/Genes: agay  
C/Superfamily: fructose-bisphosphate aldolase II  
C/Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 89.7%; Score 26; DB 2; Length 286;  
Best Local Similarity 83.3%; Pred. No. 89;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
DB 41 MRSPVI 46

## RESULT 9

E72057  
ferrochelatase CP0144 [imported] - Chlamydia pneumoniae (strains CWL029 and AR39)  
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C/Accession: E72057; F81609  
R/Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
Nature Genet. 21, 385-389, 1999  
A/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A/Reference number: A72000; PMID:9920606; PMID:10192388  
A/Accession: E72057  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-327 <ARN>  
A/Cross-references: UNIPROT:Q927V1; GB:AE001645; GB:AE001363; NID:G4376896; PIDN:AMD1874  
A/Experimental source: strain CWL029  
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,  
C.; Dodson, R.; Gilm, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A/Title: Genome sequences of Chlamydia trachomatis MoDn and Chlamydia pneumoniae AR39.  
A/Reference number: AB1500; PMID:20150255; PMID:10684935  
A/Accession: F81609  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-327 <RBA>  
A/Cross-references: GB:AE002175; GB:AE002161; NID:G7189069; PIDN:AAF38026.1; PID:G718907  
A/Experimental source: strain AR39, HL cells  
C/Genetics:  
A/Genes: hemz; CP0144

C/Superfamily: ferrochelatase

Query Match 89.7%; Score 26; DB 2; Length 327;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
DB 86 LRAPVI 91

## RESULT 10

H86565  
ferrochelatase [imported] - Chlamydia pneumoniae (strain J138)  
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C/Accession: H86565  
R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I  
Nucleic Acids Res. 28, 2311-2314, 2000  
A/Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
A/Reference number: A86491; PMID:20330349; PMID:10871362  
A/Accession: H86565  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-327 <STO>  
A/Cross-references: UNIPROT:Q927V1; GB:BA000008; NID:G8978975; PIDN:BA098810.1; GSPDB:G  
A/Experimental source: strain J138  
C/Genetics:  
A/Genes: hemz

Query Match 89.7%; Score 26; DB 2; Length 327;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
DB 86 LRAPVI 91

## RESULT 11

S13730  
pmbA protein - Escherichia coli (strain K-12)  
C/Species: Escherichia coli  
C/Date: 29-Jan-1999 #sequence\_revision 29-Jan-1999 #text\_change 09-Jul-2004  
C/Accession: S13730; S56461; F65235  
R/Rodriguez-Sainz, M.C.; Hernandez-Chico, C.; Moreno, F.  
Mol. Microbiol. 4, 1921-1932, 1990  
A/Title: Molecular characterization of pmbA, an Escherichia coli chromosomal gene requi  
A/Reference number: S13730; PMID:91186828; PMID:2082149  
A/Accession: S13730  
A/Molecule type: DNA  
A/Residues: 1-450 <ROD>  
A/Cross-references: UNIPROT:P24231; EMBL:X54152; NID:G942439; PIDN:CAA38091.1; PID:G42444  
R/Burland, V.; Plunkett III, G.; Sofia, H.D.; Daniels, D.L.; Blattner, F.R.  
Nucleic Acids Res. 23, 2105-2119, 1995  
A/Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92  
A/Reference number: S56314; PMID:95354362; PMID:7610060  
A/Accession: S56461  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-450 <BUR>  
A/Cross-references: EMBL:U14003; NID:G1263172; PIDN:AA97132.1; PID:G537077  
A/Note: The nucleotide sequence was submitted to the EMBL Data Library, August 1994  
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A/Title: The complete genome sequence of Escherichia coli K-12.  
A/Reference number: A64720; PMID:9742617; PMID:9278503  
A/Accession: F65235  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-450 <BLAT>  
A/Cross-references: GB:AE000494; GB:U00096; NID:G1790670; PIDN:AACT7192.1; PID:G1790682

A:Experimental source: strain K-12, substrain MG1655  
 C:Genetics:  
 A:Gene: pmbA  
 A:Map position: 96 min  
 C:Superfamily: Escherichia coli pmbA protein

Query Match 89.7%; Score 26; DB 1; Length 450;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
 Db 242 MKAPVI 247

# RESULT 12

AE1056  
 Probable pmbA protein pmbA [imported] - Salmonella enterica subsp. enterica serovar Typh  
 C:Species: Salmonella enterica subsp. enterica serovar Typh  
 A:Note: this species has also been called Salmonella typhi  
 C>Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C:Accession: AE1056

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; T.; Connor, P.; Cronin, A.; Davis, P.; Davies, K.M.; Dowd, L.; White, N.; Farrar, S.; Mout, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001  
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
 A:Reference number: AB0502; MUID:21534947; PMID:11677608  
 A:Accession: AE1056  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-450 <PAR>  
 A:Cross-references: GB:AL513382; PIDN:CAD06898.1; PID:G1505546; GSPDB:GN00176  
 C:Genetics:  
 A:Gene: pmbA  
 C:Superfamily: Escherichia coli pmbA protein

Query Match 89.7%; Score 26; DB 2; Length 450;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
 Db 242 MKAPVI 247

# RESULT 13

D86121  
 maturation of antibiotic McCB17, see tld genes [imported] - Escherichia coli (strain O15  
 C:Species: Escherichia coli  
 C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C:Accession: D86121

R:Perma, N.T.; Plummett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouls, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: AB5480; MUID:21074935; PMID:11206551  
 A:Accession: D86121  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-450 <STO>  
 A:Cross-references: UNIPROT:P24231; GB:AE005174; NID:G12519236; PIDN:AAG59432.1; GSPDB:G  
 A:Experimental source: strain O157:H7, substrain EBL933  
 C:Genetics:  
 A:Gene: pmbA  
 C:Superfamily: Escherichia coli pmbA protein

Query Match 89.7%; Score 26; DB 2; Length 450;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6

Db 242 MKAPVI 247

# RESULT 14

D91280  
 maturation of antibiotic McCB17 [imported] - Escherichia coli (strain O157:H7, substrain  
 C:Species: Escherichia coli  
 C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
 C:Accession: D91280

R:Hayashi, T.; Makino, K.; Ohishi, M.; Kuokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G  
 Gasaawa, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shingawa, H.  
 DNA Res. 8, 11-22, 2001  
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
 A:Reference number: A99629; MUID:21156231; PMID:11258796  
 A:Accession: D91280  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-450 <HAV>  
 A:Cross-references: UNIPROT:P24231; GB:BA000007; PIDN:BAH38635.1; PID:G13364689; GSPDB:G  
 A:Experimental source: strain O157:H7, substrain RIMD 0509952  
 C:Genetics:  
 A:Gene: EGS5212  
 C:Superfamily: Escherichia coli pmbA protein

Query Match 89.7%; Score 26; DB 2; Length 450;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6  
 Db 242 MKAPVI 247

# RESULT 15

T24916  
 hypothetical protein T14G10.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T24916

R:Wild, A.  
 submitted to the EMBL Data Library, January 1996  
 A:Reference number: Z19954  
 A:Accession: T24916  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-138 <WIL>  
 A:Cross-references: UNIPROT:Q22499; EMBL:Z68880; PIDN:CAA93096.1; GSPDB:GN00022; CESP:T  
 A:Experimental source: clone T14G10  
 A:Gene: CESP:T14G10.4  
 A:Map position: 4  
 A:Insertions: 52/3; 108/2

Query Match 86.2%; Score 25; DB 2; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 5  
 Db 1 MRAPV 5

Search completed: April 25, 2005, 20:24:08  
 Job time : 2.6918 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:10:00 ; Search time 3.09978 Seconds  
(without alignments)  
991.192 Million cell updates/sec

Title: US-10-029-926D-8  
Perfect score: 29  
Sequence: 1 MRAPV1 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	249	Q9A2W4	Q9A2W4 caulobacter
2	29	100.0	309	Q63ZV1	Q63ZV1 mus musculu
3	29	100.0	442	Q53093	Q53093 rhodobacter
4	29	100.0	442	Q53153	Q53153 rhodobacter
5	29	100.0	629	Q61371	Q61371 caenorhabdi
6	29	100.0	939	Q6PD31	Q6PD31 mus musculu
7	29	100.0	947	Q80T16	Q80T16 mus musculu
8	28	96.6	164	RHBI_PAT	RHBI_PAT
9	28	96.6	231	Q6PD44	Q6PD44 acinetobact
10	28	96.6	373	RHBI_MOUSE	RHBI_MOUSE
11	28	96.6	376	Q8P9F5	Q8P9F5 xanthomonas
12	28	96.6	425	YTR1_EBV	YTR1_EBV
13	28	96.6	425	Q777C1	Q777C1 human herpe
14	28	96.6	438	RHBI_HUMAN	RHBI_HUMAN
15	28	96.6	541	Q8NT69	Q8NT69 corynebacte
16	28	96.6	577	Q8CTG6	Q8CTG6 Kluveromye
17	28	96.6	713	Q7Y7Y3	Q7Y7Y3 cryptospori
18	27	93.1	247	Q27295	Q27295 methanobact
19	27	93.1	376	Q9L778	Q9L778 xanthomonas
20	27	93.1	376	Q8PL69	Q8PL69 xanthomonas
21	27	93.1	416	Q9AC09	Q9AC09 streptomyce
22	27	93.1	449	Q89X81	Q89X81 bradyrhizob
23	27	93.1	535	1 TLE1_BRARE	1 TLE1_BRARE
24	27	93.1	771	Q98TH2	Q98TH2 brachydania
25	26	89.7	162	Q8ILB7	Q8ILB7 plasmodium
26	26	89.7	162	Q7RL13	Q7RL13 plasmodium
27	26	89.7	199	Q6BSE3	Q6BSE3 debaromyce
28	26	89.7	250	1 PDXO_BRAJA	1 PDXO_BRAJA
29	26	89.7	264	Q7F2A7	Q7F2A7 oryza sativ
30	26	89.7	286	1 AGAY_ECOLI	1 AGAY_ECOLI
31	26	89.7	286	Q9K1F8	Q9K1F8 escherichia

## ALIGNMENTS

RESULT 1		ALIGNMENTS	
Q9A2W4	PRELIMINARY;	PRT;	249 AA.
AC Q9A2W4;			
DT 01-JUN-2001 (Tremblrel. 17, Created)			
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)			
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE Hydrolyase, alpha/beta hydrolase fold family.			
GN OrderedLocustNames=CC3442;			
OS Caulobacter crescentus.			
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;			
OC Caulobacteraceae; Caulobacter.			
OX NCBI_TaxID=155892;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=ATCC 19089 / CB15;			
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;			
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.B.,			
RA Bisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,			
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,			
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,			
RA Kolonay J.F., Smit J., Craven M.B., Knout H.M., Shetty J.,			
RA Berry K.J., Uteirack T.R., Tran K., Wolf A.M., Vamathevan J.J.,			
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,			
RA Fraser C.M.;			
RT "Complete genome sequence of Caulobacter crescentus.";			
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).			
DR EMBL: A8006003; AAK25404.1; -.			
DR TIG: H87675; H87675.			
DR PIR: CC3442; -.			
DR GO: GO:0016787; F:hydrolase activity; IEA.			
DR CO: GO:006725; P:aromatic compound metabolism; IEA.			
DR InterPro: IPR000073; A/B_hydrolase.			
DR InterPro: IPR003089; AB_hydrolase.			
DR InterPro: IPR000379; Ser_esterase.			
DR Pfam: PF00561; ABhydrolase.1; 1.			
DR PRINTS: PR00111; ABHYDROLASE.			
KW Complete proteome; Hydrolase.			
SQ SEQUENCE 249 AA; 26772 MW; 491350127DD300AE CRC64;			
Query Match 100.0%; Score 29; DB 2; Length 249;			
Best Local Similarity 100.0%; Pred. No. 65;			
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1 MRAPV1 6			
Db 1 MRAPV1 6			
RESULT 2			
Q63ZV1	PRELIMINARY;	PRT;	309 AA.
ID Q63ZV1;			
AC Q63ZV1;			
DT 25-OCT-2004 (Tremblrel. 28, Created)			

DT 25-OCT-2004 (TREMblrel. 28, last sequence update)  
 DT 25-OCT-2004 (TREMblrel. 28, last annotation update)  
 DE Hypothetical protein (Fragment).  
 OC Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxId=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Mouse;  
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,  
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Mouse;  
 RA Director MGC Project;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC082807; AA82807.1; -.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 309 AA; 32959 MW; 5F551A9B90CC8714 CRC64;  
 Query Match 100.0%; Score 29; DB 2; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 82;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRAPIV 6  
 Db 286 MRAPIV 291  
 RESULT 3  
 Q53093 PRELIMINARY; PRT; 442 AA.  
 AC Q53093;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)  
 DE Flii.  
 GN Name=flii;  
 OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
 OC Rhodobacteraceae; Rhodobacter.  
 ON NCBI\_TaxId=1063;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=2.4.1;  
 RX MEDLINE=96200857; PubMed=8621091; DOI=10.1016/0378-1119(95)00855-1;  
 RA Ballado T., Campos A., Camarena L., Dreyfus G.;  
 RT "Flaegellar genes from Rhodobacter sphaeroides are homologous to genes  
 of the flif operon of Salmonella typhimurium and to the type-III  
 secretion system.";  
 RL Gene 170:69-72(1996).  
 CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.

DR EMBL; U31090; AAB07344.1; -.  
 DR PIR; JC4733; JC4733.  
 DR HSSP; P03002; 1PVO.  
 DR GO; GO:0005737; C:cytoplasm; IEA.  
 DR GO; GO:0014669; C:proton-transporting two-sector ATPase complex; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0016887; F:ATPase activity; IEA.  
 DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.  
 DR GO; GO:0046961; F:hydrogen-transporting ATPase activity; IEA.  
 DR GO; GO:0016787; F:hydrolyase activity; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR GO; GO:0019986; F:ATP synthase coupled proton transport; IEA.  
 DR GO; GO:0009058; F:biogenesis; IEA.  
 DR GO; GO:0006811; P:ion transport; IEA.  
 DR GO; GO:0015031; P:protein transport; IEA.  
 DR InterPro; IPR003593; AAA ATPase.  
 DR InterPro; IPR000194; ATPase\_a/bcentre.  
 DR InterPro; IPR004100; ATPase\_a/b\_N.  
 DR InterPro; IPR005714; Flii\_YscN.  
 DR Pfam; PF00006; ATP-synt\_ab; 1.  
 DR SMART; SM00382; AAA; 1.  
 DR TIGRFAMs; TIGR01026; Flii\_YscN; 1.  
 DR PROSITE; PS00152; ATPASE\_ALPHA\_BETA; UNKNOWN\_1.  
 KW ATP synthase; ATP-binding; Hydrolyase; ion transport; Transport.  
 SQ SEQUENCE 442 AA; 46852 MW; E6D35531F5A59BAE CRC64;  
 Query Match 100.0%; Score 29; DB 2; Length 442;  
 Best Local Similarity 100.0%; Pred. No. 1,2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRAPIV 6  
 Db 77 MRAPIV 82  
 RESULT 4  
 Q53153 PRELIMINARY; PRT; 442 AA.  
 AC Q53153;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)  
 DE Flii protein.  
 GN Name=flii;  
 OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
 OC Rhodobacteraceae; Rhodobacter.  
 ON NCBI\_TaxId=1063;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WS8;  
 RX MEDLINE=96377148; PubMed=8759796; DOI=10.1016/0378-1097(96)00252-2;  
 RA Goodfellow I.G., Pollitt C.E., Sockett R.E.;  
 RT "Cloning of the flii gene from Rhodobacter sphaeroides WS8 by analysis  
 of a transposon mutant with impaired motility.";  
 RL FEMS Microbiol. Lett. 142:111-116(1996).  
 CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.  
 DR EMBL; X97201; CA65834.1; -.  
 DR HSSP; P03002; 1PVO.  
 DR GO; GO:0005737; C:cytoplasm; IEA.  
 DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0016887; F:ATPase activity; IEA.  
 DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.  
 DR GO; GO:0046961; F:hydrogen-transporting ATPase activity; IEA.  
 DR GO; GO:0016787; F:hydrolyase activity; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR GO; GO:0019986; F:ATP synthase coupled proton transport; IEA.  
 DR GO; GO:0009058; F:biogenesis; IEA.  
 DR GO; GO:0006811; P:ion transport; IEA.  
 DR GO; GO:0015031; P:protein transport; IEA.  
 DR InterPro; IPR003593; AAA ATPase.  
 DR InterPro; IPR000194; ATPase\_a/bcentre.

DR InterPro: IPR004100; ATPase\_a/b\_N.  
DR InterPro: IPR005714; F111\_YscN.  
DR Pfam: PF00006; ATP-8ynt\_ab; 1.  
DR SMART: SM00382; AAA; 1.  
DR TIGRfam: TIGR01026; f111\_YscN; 1.  
DR PROSITE: PS00152; ATPase\_ALPHA\_BETA; UNKNOWN 1.  
DR ATP synthetase; ATP-binding; Hydrolase; Ion transport; Transport.  
SQ SEQUENCE 442 AA; 46813 MW; AD070DA817FD3CC3 CRC64;  
  
Query Match 100.0%; Score 29; DB 2; Length 442;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MRAPVI 6  
Db 77 MRAPVI 82  
  
RESULT 5  
061371 PRELIMINARY; PRT; 629 AA.  
ID 061371; O9TKY7.  
AC 061371-1998 (TReMBLrel. 07, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
DE Acetylcholinesterase (EC 3.1.1.7) (Abnormal acetylcholinesterase  
protein 2).  
GN Name=ace-2; ORFNames=Y44E3A.2;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=N2;  
RA MEDLINE=98198570; PubMed=9539167; DOI=10.1016/S0014-5793(98)00191-4;  
RX Grauso M., Culetto E., Combes D., Fedon Y., Tountant J.P., Arpagaus M.;  
RT "Existence of four acetylcholinesterase genes in the nematodes  
Caenorhabditis elegans and Caenorhabditis briggsae.";   
FEBS Lett. 424:279-284(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=N2;  
RA Grauso M., Culetto E., Fedon Y., Combes D., Tountant J.P., Arpagaus M.;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Br1etol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RG Wormbase Consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for  
investigating biology. The C. elegans Sequencing Consortium.";   
Science 282:2012-2018(1998).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Br1etol N2;  
RA Moesener J., Graves T., Keppler D.;  
RT "The sequence of C. elegans comid Y44E3A.";   
Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Br1etol N2;  
RA Waterston R.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Br1etol N2;  
RA Wilson R.;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Br1etol N2;  
RG Wormbase Consortium;

RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
DR EMBL: AF025378; AAC14016.2; -  
DR EMBL: AF065689; AAC78228.2; -  
DR PIR: T33842; T33842.  
DR PIR: T37255; T37255.  
DR HSSP: P06276; 1P0P.  
DR Wormbase: WBGene0000036; ace-2.  
DR WormPep: Y44E3A.2; CE28363.  
DR GO: GO:0003990; F:acetylcholinesterase activity; IEA.  
DR GO: GO:0004104; F:cholinesterase activity; IEA.  
DR GO: GO:0016787; F:hydrolase activity; IEA.  
DR InterPro: IPR002018; Carboxylesterase.  
DR InterPro: IPR000997; Cholinesterase.  
DR InterPro: IPR000379; Ser esters.  
DR Pfam: PF00035; Coesterase; 1.  
DR PRINTS: PR00878; CHOLINESTRASE.  
DR PROSITE: PS00122; CARBOXYLESTERASE\_\_B\_1; 1.  
KW Hydrolase.  
SQ SEQUENCE 629 AA; 70863 MW; 74940F512FEDF869 CRC64;  
  
Query Match 100.0%; Score 29; DB 2; Length 629;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MRAPVI 6  
Db 1 MRAPVI 6  
  
RESULT 6  
06PD31 PRELIMINARY; PRT; 939 AA.  
ID 06PD31;  
AC 06PD31-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Donald M.P., Caesavant T.L., Schetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Miliady S.J.,  
RA Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gurnatone P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Whiting J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakeley R.W., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Rodriguez A.C., Touchman J., Green B.D., Dickson M.C.,  
RA Krzywinski M.I., Skalka U., Smalls D.E., Schmeich A., Schein J.B.,  
RA Jones S.J., Matra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";   
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC058971; AAH58971.1; -  
DR InterPro: IPR006933; HAP1\_N.

DR InterPro; IPR000585; Hemopexin.  
 DR InterPro; IPR010978; tRNA\_binding\_arm.  
 DR Pfam; PF04849; HAP1.N.1.  
 DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 939 AA; 104466 MW; 64B1D5D34DF36FCB CRC64;

Query Match 100.0%; Score 29; DB 2; Length 939;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPIV 6  
 |||||  
 DB 916 MRAPIV 921

RESULT 7  
 Q80TL6 PRELIMINARY; PRT; 947 AA.

AC Q80TL6; (T-EMBLrel. 24, Created)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (T-EMBLrel. 26, Last annotation update)  
 DE KIAA1042 protein (Fragment).  
 GN Name=KIAA1042;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22579291; PubMed=12693553;  
 RA Okazaki N., Kikuno R., Ohara R., Iamoro S., Aizawa H., Yuasa S.,  
 Nakajima D., Nagase T., Ohara O., Koga H.;  
 RT "Prediction of the coding sequences of mouse homologues of KIAA gene:  
 RT 11. The complete nucleotide sequences of 400 mouse KIAA-homologous  
 RT cDNAs identified by screening of terminal sequences of cDNA clones  
 RT randomly sampled from size-fractionated libraries.";  
 RL DNA Res. 10:35-48(2003).

DR EMBL; AK122426; BC65708.1; -;  
 DR GO; GO:0005634; C:nucleus; ISS.  
 DR GO; GO:0005886; C:plasma membrane; ISS.  
 DR GO; GO:0005515; F:protein binding; ISS.  
 DR GO; GO:0005102; F:receptor binding; ISS.  
 DR GO; GO:0006493; P:O-linked glycosylation; ISS.  
 DR GO; GO:0006005; P:protein targeting; ISS.  
 DR InterPro; IPR006933; HAP1.N.  
 DR InterPro; IPR00585; Hemopexin.  
 DR InterPro; IPR010978; tRNA\_binding\_arm.  
 DR Pfam; PF04849; HAP1.N.1.  
 DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN\_1.  
 FT NON\_TER 1  
 SQ SEQUENCE 947 AA; 105486 MW; 0987284C6ACF23A5 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 947;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPIV 6  
 |||||  
 DB 924 MRAPIV 929

RESULT 8  
 RHBI\_RAT STANDARD; PRT; 164 AA.

AC Q88779;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Rhomboid-related protein 1 (BC 3.4.21.-) (RRP) (rhomboid-like protein

DE 1) (Fragment).  
 GN Name=Rhbdl1; Synonyms=Rhbdl;  
 GN Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Intestinal epithelium;  
 RX MEDLINE=98324821; PubMed=9662444; DOI=10.1016/S0014-5793(98)00622-X;

RA Pascall J.C., Brown K.D.;  
 RT "Characterization of a mammalian cDNA encoding a protein with high  
 RT sequence similarity to the Drosophila regulatory protein Rhomboid.";  
 RL FEBS Lett. 429:337-340(1998).

CC -1- FUNCTION: May be involved in regulated intramembrane proteolysis  
 CC and the subsequent release of functional polypeptides from their  
 CC membrane anchors (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to the peptidase S54 family.

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DR EMBL; Y17258; CAA76716.1; -;

DR MEROPS; S54.005; -;  
 DR InterPro; IPR002610; Rhomboid\_like.

DR Pfam; PF01694; Rhomboid; 1.  
 KW Hydrolase; Protease; Serine protease; Transmembrane.

FT NON\_TER 1  
 FT TRANSMEM 10 30 Potential.  
 FT TRANSMEM 32 52 Potential.  
 FT TRANSMEM 56 76 Potential.  
 FT TRANSMEM 120 140 Potential.  
 FT ACT SITE 60 60 Charge relay system (By similarity).  
 FT ACT SITE 125 125 Charge relay system (By similarity).  
 FT NON\_TER 164  
 SQ SEQUENCE 164 AA; 17662 MW; CF62ACB3BC99210 CRC64;

Query Match 96.6%; Score 28; DB 1; Length 164;  
 Best Local Similarity 83.3%; Pred. No. 76;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPIV 6  
 |||||  
 DB 52 MRAPIV 57

RESULT 9  
 Q6FD44 PRELIMINARY; PRT; 231 AA.

ID Q6FD44;  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)

DE Hypothetical protein.  
 GN OrderedLocNames=AC1AD1133;  
 OS Acinetobacter sp. (strain ADP1).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Moraxellaceae; Acinetobacter.  
 NCBI\_TaxID=62977;

RN [1]  
 RP SEQUENCE FROM N.A.

RA Barbe V., Vallienet D., Fonknechten N., Kreimeyer A., Oztas S.,  
 RA Labarre L., Crivellier S., Robert C., Duprat S., Wincker P.,  
 RA Orsillon L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;  
 RT "Unique features revealed by the genome sequence of Acinetobacter sp.  
 RT ADP1, a versatile and naturally transformation competent bacterium.";  
 RT Nucleic Acids Res. 0:0-0(2004).



DR EMBL; CR543861; CAG68015.1; -  
 DR InterPro; IPR007055; TAD.  
 DR Pfam; PF04972; BON; 1.  
 DR PROSITE; PSS0914; BON; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 231 AA; 24680 MW; 7FCDAFCADF5E319F CRC64;

Query Match 96.6%; Score 28; DB 2; Length 231;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 6  
 |||||  
 Db 136 MRAPV 141

RESULT 10  
 ID RBH1\_MOUSE STANDARD; PRT; 373 AA.  
 AC 08VC82;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Rhomboid-related protein 1 (EC 3.4.21.-) (RRP) (Rhomboid-like protein 1).  
 GN Name=Rhbd1; Synonym=Rhbd1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Retina;  
 RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;  
 RA Klanner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;  
 RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;  
 RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Haileh F.;  
 RA Diatchenko L.; Matsushita K.; Parker A.F.; Rubin G.M.; Hong L.;  
 RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Schetz T.E.;  
 RA Brownstein M.U.; Ueda T.B.; Toshiyuki S.; Carninci P.; Prange C.;  
 RA Raha S.S.; Loughellano N.A.; Peters G.J.; Abramson R.D.; Mulyahy S.J.;  
 RA Bosak S.A.; McMan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;  
 RA Richards S.; Morley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulik S.W.;  
 RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;  
 RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;  
 RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;  
 RA Butlerfield Y.S.N.; Krzywicki M.I.; Skalska U.; Smalins D.E.;  
 RA Scherch A.; Schein U.E.; Jones S.U.M.; Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: May be involved in regulated intramembrane proteolysis  
 CC and the subsequent release of functional polypeptides from their  
 CC membrane anchors (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -1- SIMILARITY: Belongs to the peptidase S54 family.  
 CC -----  
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 CC -----  
 DR EMBL; BC021549; AAH21549.1; -  
 DR MEROPS; S54.005; -  
 DR MGD; MGI:2384891; Rhbd1.  
 DR InterPro; IPR002048; EF\_Hand.  
 DR InterPro; IPR010983; EF\_Hand\_like.

DR InterPro; IPR002610; Rhomboid-like.  
 DR Pfam; PF01694; Rhomboid; 1.  
 KW Hydrolase; Protease; Serine protease; Transmembrane.  
 DR TRANSMEM 131 151  
 FT TRANSMEM 196 216  
 FT TRANSMEM 219 239  
 FT TRANSMEM 243 263  
 FT TRANSMEM 275 294  
 FT TRANSMEM 307 327  
 FT TRANSMEM 340 360  
 FT ACT SITE 199 199  
 FT ACT SITE 247 247  
 FT ACT SITE 312 312  
 SQ SEQUENCE 373 AA; 41766 MW; 1FAE538B3A363D2A CRC64;

Query Match 96.6%; Score 28; DB 1; Length 373;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 6  
 |||||  
 Db 239 MRAPV 244

RESULT 11  
 ID O8P9F5 PRELIMINARY; PRT; 376 AA.  
 AC O8P9F5;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Flagellar protein.  
 GN Name=flhB; OrderedLocNames=XCC1910;  
 OS Xanthomonas campestris (pv. campestris).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xanthomonas.  
 OX NCBI\_Taxid=340;  
 [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 33913 / NCPPB 528;  
 RA MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;  
 RA da Silva A.C.R.; Ferro J.A.; Reinach F.C.; Parah C.S.; Furlan L.R.;  
 RA Oleggio R.B.; Monteiro-Vitorello C.B.; Van Sluys M.A.; Almeida N.F.;  
 RA Alves L.M.C.; do Amaral A.M.; Bertolini M.C.; Camargo L.E.A.;  
 RA Camarotte G.; Camaral F.; Cardozo J.; Chamberg F.; Clapina L.P.;  
 RA Ciccarelli R.M.B.; Coutinho L.L.; Cursino-Santos J.R.; El-Dorri H.;  
 RA Faria J.B.; Ferreira A.J.S.; Ferreira R.C.C.; Ferro M.I.T.;  
 RA Formighieri E.F.; Franco M.C.; Greggio C.C.; Gruber A.;  
 RA Katsuyama A.M.; Kishi L.T.; Leite R.P.; Lemos B.G.M.; Lemos M.V.F.;  
 RA Locali E.C.; Machado M.A.; Madeira A.M.B.N.; Martinez-Rossi N.M.;  
 RA Martins E.C.; Melandri J.; Menck C.F.M.; Miyaki C.Y.; Moon D.H.;  
 RA Moreira L.M.; Novo M.T.M.; Okura V.K.; Oliveira M.C.; Oliveira V.R.;  
 RA Pereira H.A.; Rossi A.; Sena J.A.D.; Silva C.; de Souza R.F.;  
 RA Spindola L.A.F.; Takita M.A.; Tamura R.E.; Teixeira E.C.; Tezza R.I.D.;  
 RA Trindade dos Santos M.; Truffi D.; Tsai S.M.; White F.F.;  
 RA Setubal J.C.; Kitajima J.P.P.  
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing  
 RT host specificities.";  
 RT Nature 417:459-463(2002).  
 DR EMBL; AB012294; AAH4119.1; -  
 DR GO; GO:0016020; C-membrane; IEA.  
 DR GO; GO:0009306; P-protein secretion; IEA.  
 DR InterPro; IPR006135; Bac\_Export\_2.  
 DR InterPro; IPR006136; FlhB.  
 DR Pfam; PF01312; Bac\_export\_2; 1.  
 DR PRINTS; PRO0950; TYP31MSPROT.  
 DR TIGRPFAM; TIGR00328; flhB; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 376 AA; 41490 MW; 406778385A158910 CRC64;  
 Query Match 96.6%; Score 28; DB 2; Length 376;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV1 6  
 DB 285 MRAPV 290

RESULT 12  
 YTRL EBV STANDARD; PRT; 425 AA.  
 ID YTRL EBV  
 AC P30119;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Hypothetical BTRF1 protein.  
 GN Name=BTRF1;  
 OS Epstein-Barr virus (strain B95-8) (HHV-4) (Human herpesvirus 4).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Gammaherpesvirinae; Lymphocryptovirus.  
 OX NCBI\_TaxID=10377;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=84270667; PubMed=6087149;  
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,  
 RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,  
 RA Tufnell P.S., Barrell B.G.;  
 RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";  
 RL Nature 310:207-211(1984).  
 CC -1- SIMILARITY: Belongs to the herpesviruses BTRF1 family.  
 CC -----  
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 CC -----  
 CC DR EMBL; V01555; CAA24796.1; -.  
 CC DR PIR; S33045; S33045.  
 CC DR InterPro; IPR006772; Herpes\_BTRF1.  
 CC DR Pfam; PF04682; Herpes\_BTRF1; 1.  
 CC KW Hypothetical protein.  
 CC SQ SEQUENCE 425 AA; 46711 MW; 0ECBESFPD30495BD CRC64;

Query Match 96.64; Score 28; DB 1; Length 425;  
 Best Local Similarity 83.3%; Pctd. No. 2.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV1 6  
 DB 87 MRAPV1 92

RESULT 13  
 Q777C1 PRELIMINARY; PRT; 425 AA.  
 ID Q777C1  
 AC Q777C1;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE BTRF1 protein (Fragment).  
 GN Name=BTRF1;  
 OS Human herpesvirus 4 (Epstein-Barr virus).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Gammaherpesvirinae; Lymphocryptovirus.  
 OX NCBI\_TaxID=10376;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RC MEDLINE=84270667; PubMed=6087149;  
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,  
 RA Gibson T.J., Hatfull G.F., Hudson G.S., Satchwell S.C., Seguin C.,  
 RA Tufnell P.S., Barrell B.G.;

RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";  
 RL Nature 310:207-211(1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RC MEDLINE=88283646; PubMed=2840285;  
 RA Laux G., Perricaudet M., Farrell P.J.;  
 RT "A spliced Epstein-Barr virus gene expressed in immortalized  
 RT lymphocytes is created by circularization of the linear viral  
 RT genome.";  
 RL EMBO J. 7:769-774(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RC MEDLINE=82014887; PubMed=6269068;  
 RA Arrand J.R., Rymo L., Walsh J.E., Bjorck E., Lindahl T., Griffin B.E.;  
 RT "Molecular cloning of the complete Epstein-Barr virus genome as a set  
 RT of overlapping restriction endonuclease fragments.";  
 RL Nucleic Acids Res. 9:2999-3014(1981).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RC MEDLINE=82059504; PubMed=7301588;  
 RA Kozak M.;  
 RT "Possible role of flanking nucleotides in recognition of the AUG  
 RT initiator codon by eukaryotic ribosomes.";  
 RL Nucleic Acids Res. 9:5233-5252(1981).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RC MEDLINE=83109311; PubMed=6296170;  
 RA Deininger P.L., Bankier A., Farrell P., Baer R., Barrell B.;  
 RT "Sequence analysis and in vitro transcription of portions of the  
 RT Epstein-Barr virus genome.";  
 RL J. Cell. Biochem. 19:267-274(1982).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RC MEDLINE=83169725; PubMed=6300857;  
 RA Farrell P.J., Deininger P.L., Bankier A., Barrell B.;  
 RT "Homologous upstream sequences near Epstein-Barr virus promoters.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1565-1569(1983).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RC MEDLINE=85035713; PubMed=6092825;  
 RA Bankier A.T., Deininger P.L., Farrell P.J., Barrell B.G.;  
 RT "Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8  
 RT Epstein-Barr virus.";  
 RL Mol. Biol. Med. 1:21-45(1983).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RC MEDLINE=85060424;  
 RA Seguin C., Farrell P.J., Barrell B.G.;  
 RT "DNA sequence and transcription of the BamHI fragment B region of B95-  
 RT 8 Epstein-Barr virus.";  
 RL Mol. Biol. Med. 1:369-392(1983).  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RC MEDLINE=83294686; PubMed=6310141;  
 RA Jiang K.T., Hayward S.D.;  
 RT "Organization of the Epstein-Barr virus DNA molecule. III. Location of  
 RT the p3HR-1 deletion junction and characterization of the NotI repeat  
 RT units that form part of the template for an abundant 12-O-  
 RT tetradecanoylphorbol-13-acetate-induced mRNA transcript.";  
 RL J. Virol. 48:135-148(1983).  
 RN [10]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RC MEDLINE=85060428; PubMed=6094955;  
 RA Bankier A.T., Deininger P.L., Satchwell S.C., Baer R., Farrell P.J.;

RA Barrell B.G.;  
 RT "DNA sequence analysis of the EcoRI DheI fragment of B95-8 Epstein-  
 RT Barr virus containing the terminal repeat sequences.";  
 RL Mol. Biol. Med. 1:425-445(1983).  
 [11]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RX MEDLINE=20311131; PubMed=10872327;  
 RA Farrell P.J., Bankier A., Seguin C., Deininger P., Barrell B.G.;  
 RT "Latent and lytic cycle promoters of Epstein-Barr virus.";  
 RL EMO J. 2:1331-1338(1983).  
 [12]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RX MEDLINE=84207939; PubMed=6327290;  
 RA Jones M.D., Foerster L., Sheedy T., Griffin B.E.;  
 RT "The EB virus genome in Daudi Burkitt's lymphoma cells has a deletion  
 RT similar to that observed in a non-transforming strain (P3HR-1) of the  
 RT virus.";  
 RL EMO J. 3:813-821(1984).  
 [13]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RX MEDLINE=84236104; PubMed=6203743;  
 RA Biggin M., Farrell P.J., Barrell B.G.;  
 RT "Transcription and DNA sequence of the BamHI L fragment of B95-8  
 RT Epstein-Barr virus.";  
 RL EMO J. 3:1083-1090(1984).  
 [14]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RX MEDLINE=84222045; PubMed=6328526;  
 RA Yates J., Warren N., Reisman D., Studden B.;  
 RT "A cis-acting element from the Epstein-Barr viral genome that permits  
 RT stable replication of recombinant plasmids in latently infected  
 RT cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3806-3810(1984).  
 [15]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RX MEDLINE=84247360; PubMed=6330697;  
 RA Gibson T., Stockwell P., Ginsburg M., Barrell B.;  
 RT "Homology between two EBV early genes and HSV ribonucleotide reductase  
 RT and 38k genes.";  
 RL Nucleic Acids Res. 12:5087-5099(1984).  
 [16]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RX MEDLINE=87289053; PubMed=3039467;  
 RA Bodescot M., Perricaudet M.;  
 RT "Clustered alternative splice sites in Epstein-Barr virus RNAs.";  
 RL Nucleic Acids Res. 15:5887-5887(1987).  
 [17]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RX MEDLINE=91021056; PubMed=2171209;  
 RA Parker B.D., Bankier A., Satchwell S., Barrell B., Farrell P.J.;  
 RT "Sequence and transcription of Raji Epstein-Barr virus DNA spanning  
 RT the B95-8 deletion region.";  
 RL Virology 179:339-346(1990).  
 [18]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RX MEDLINE=87289053; PubMed=3039467;  
 RA Hatfull G.F., Barrell B.G., Quinn J., McGeoch D.;  
 RT Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 [19]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B95-8;  
 RA Birne U.K., Aron W., Farrell P.J.;  
 RT "Induction of Epstein-Barr virus late promoters on small plasmids in  
 RT the EBV late lytic cycle requires ori L<sub>yt</sub>.";  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ507799; CAD53449.1; -.

DR InterPro; IPR006772; Herpes\_BTRF1.  
 DR Pfam; PF04682; Herpes\_BTRF1; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 425 425  
 SQ SEQUENCE 425 AA; 46711 MW; 0ECB55FD30495BD CRC64;  
 Query Match 96.6%; Score 28; DB 2; Length 425;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRAPVI 6  
 DB 87 MRAPVI 92  
 RESULT 14  
 ID RHB1\_HUMAN STANDARD; PRT; 438 AA.  
 AC 075783; Q9N085;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Rhomboid-related protein 1 (EC 3.4.21.-) (RRP) (Rhomboid-like protein  
 DE 1).  
 GN Name=RHBDL1; Synonyms=RHBDL;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Leukemia;  
 RX MEDLINE=98324821; PubMed=9662444; DOI=10.1016/S0014-5793(98)00622-X;  
 RA Pascall J.C., Brown K.D.;  
 RT "Characterization of a mammalian cDNA encoding a protein with high  
 RT sequence similarity to the Drosophila regulatory protein Rhomboid.";  
 RL FEBS Lett. 429:337-340(1998).  
 [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=21096910; PubMed=1115797; DOI=10.1093/hmg/10.4.339;  
 RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,  
 RA Tifarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,  
 RA Higgs D.R.;  
 RT "Sequence, structure and pathology of the fully annotated terminal 2  
 RT kb of the short arm of human chromosome 16.";  
 RL Hum. Mol. Genet. 10:339-352(2001).  
 CC -1- FUNCTION: May be involved in regulated intramembrane proteolysis  
 CC and the subsequent release of functional polypeptides from their  
 CC membrane anchors (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=O75783-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=O75783-2; Sequence=VSP\_005372;  
 CC -1- TISSUE SPECIFICITY: Detected in heart, brain, skeletal muscle and  
 CC kidney.  
 CC -1- SIMILARITY: Belongs to the peptidase S54 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; Y17108; CA76629.1; -.  
 DR EMBL; AJ72344; CAC00640.1; -.  
 DR EMBL; AE006464; AAK61241.1; -.  
 DR MEROPS; S54.005; -.  
 DR Genew; HGNC:10007; RHBDL1.

DR MIM; 603264; -  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005624; C:membrane fraction; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR002048; PF-hand\_1like.  
 DR InterPro; IPR001983; EF\_Hand\_1like.  
 DR Pfam; PF01694; Rhomboid; 1.  
 KM Alternative splicing; Hydrolase; Protease; Serine protease;  
 FT Transmembrane  
 FT TRANSMEM 196 216 Potential.  
 FT TRANSMEM 262 282 Potential.  
 FT TRANSMEM 284 304 Potential.  
 FT TRANSMEM 308 328 Potential.  
 FT TRANSMEM 340 359 Potential.  
 FT TRANSMEM 372 392 Potential.  
 FT TRANSMEM 405 425 Potential.  
 FT ACT\_SITE 264 264 Charge relay system (By similarity).  
 FT ACT\_SITE 312 312 Charge relay system (By similarity).  
 FT ACT\_SITE 377 377 Charge relay system (By similarity).  
 FT VARSPLIC 1 77 MGRVBDGTEBELDMDPGTSALPAPGKQPREOTGTGPL  
 FT DRSSLQQLIOE (in isoform 2).  
 FT /FTid=VSP\_005372.  
 SQ SEQUENCE 438 AA; 48314 MW; A7644AD3644A2F6 CRC64;  
 Query Match 96.6%; Score 28; DB 1; Length 438;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRAPVI 6  
 Db 304 MRAPV 309

RESULT 15  
 Q8NT69  
 ID Q8NT69 PRELIMINARY; PRT; 541 AA.  
 AC Q8NT69; Q6M7S9;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE ResB protein required for cytochrome c biosynthesis (Membrane protein  
 DE required for cytochrome c biosynthesis).  
 GN OorediocuNames=Cg10441, CG0523;  
 OS Corynebacterium glutamicum (Brevibacterium flavum).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
 OC NCBI\_TaxID=1718;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa;  
 RC Nakagawa S.;  
 RA "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;  
 RX PubMed=1294826; DOI=10.1016/S0168-1656(03)00154-8;  
 RA Kallinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,  
 RA Burkovski A., Busch N., Eggeling L., Eikmanns B.J., Galgatal L.,  
 RA Goessmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,  
 RA McHardy A.C., Meyer F., Moeckel B., Pfeifferle W., Puhler A.,  
 RA Rey D.A., Rueckert C., Rupp O., Sahn H., Wendisch V.F., Wiegand I.,  
 RA Tauch A.;  
 RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence  
 RT and its impact on the production of L-aspartate-derived amino acids  
 RT and vitamins.";  
 RL J. Biotechnol. 104:5-25 (2003).  
 DR EMBL; AP005275; BAB97834.1; -  
 DR EMBL; BX927149; CAF19157.1; -  
 DR InterPro; IPR007816; ResB.  
 DR Pfam; PF05140; ResB; 1.

KW Complete proteome.  
 SQ SEQUENCE 541 AA; 61244 MW; 37F42BA0A74F78BB CRC64;  
 Query Match 96.6%; Score 28; DB 2; Length 541;  
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRAPVI 6  
 Db 103 MRAPV 108

Search completed: April 25, 2005, 20:33:58  
 Job time : 5.09978 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: April 25, 2005, 20:24:31 ; Search time 17.1053 Seconds

(without alignments)  
484.413 Million cell updates/sec

Title: US-10-029-926D-7

Perfect score: 576  
Sequence: 1 SELTOPPAVSVALGQTVRIT.....SGNHVFGGKTLTVLGAA 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PCITUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Match	Query Length	DB ID	Description
1	576	100.0	278	3	US-09-260-527-3
2	576	100.0	280	3	US-09-260-527-1
3	576	100.0	309	3	US-09-079-029-9
4	576	100.0	312	3	US-09-079-029-10
5	558	96.9	111	4	US-09-720-493-4
6	554	96.2	109	2	US-09-203-768A-8
7	537	93.2	109	2	US-08-652-816A-16
8	531.5	92.3	109	2	US-08-665-202-34
9	531.5	92.3	109	4	US-09-315-574-34
10	525	91.1	101	4	US-09-726-219A-168
11	502	87.2	97	2	US-08-665-202-35
12	502	87.2	97	4	US-09-315-574-35
13	494.5	85.9	104	3	US-08-793-450-6
14	494.5	85.9	104	3	US-08-793-450-6
15	487	84.5	104	3	US-09-240-374-49
16	480	83.3	106	3	US-09-240-374-48
17	475.5	82.6	102	4	US-09-726-219A-174
18	473	82.1	106	3	US-09-240-374-47
19	473	82.1	106	3	US-09-240-374-47
20	471	81.8	103	2	US-08-273-146-71
21	448.5	77.9	108	3	US-09-025-769B-20
22	448.5	77.9	108	4	US-09-490-070A-20
23	448.5	77.9	108	4	US-09-490-153-20
24	448.5	77.9	108	4	US-09-490-324-20
25	443.5	77.0	105	1	US-08-488-113B-157
26	443.5	77.0	105	1	US-08-477-484B-157
27	443.5	77.0	105	1	US-08-107-669D-21

28	443.5	77.0	105	1	US-08-472-788A-21	Sequence 21, Appl
29	443.5	77.0	105	2	US-08-477-531B-21	Sequence 21, Appl
30	443.5	77.0	105	2	US-08-646-360-157	Sequence 157, Appl
31	443.5	77.0	105	2	US-08-082-842A-21	Sequence 21, Appl
32	443.5	77.0	105	3	US-08-839-765-157	Sequence 157, Appl
33	443.5	77.0	105	3	US-09-136-389-157	Sequence 157, Appl
34	443.5	77.0	105	3	US-09-610-838-157	Sequence 157, Appl
35	443.5	77.0	105	4	US-09-711-485-157	Sequence 157, Appl
36	441	76.6	125	4	US-09-471-276-1249	Sequence 1249, Ap
37	423	73.4	108	1	US-08-360-125-12	Sequence 12, Appl
38	423	73.4	108	2	US-08-450-578-12	Sequence 12, Appl
39	423	73.4	108	2	US-09-017-628-12	Sequence 12, Appl
40	423	73.4	108	2	US-09-014-880-12	Sequence 12, Appl
41	423	73.4	108	4	US-08-450-363-12	Sequence 12, Appl
42	423	73.4	108	4	US-09-467-903-12	Sequence 12, Appl
43	420	72.9	118	4	US-09-513-999C-4175	Sequence 4175, Ap
44	419	72.7	109	3	US-09-157-370-5	Sequence 5, Appl1
45	397	68.9	107	3	US-09-025-769B-34	Sequence 34, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikelsen, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260.527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0.
; SEQ ID NO 3
; LENGTH: 278
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
; OTHER INFORMATION: from a naive phase display library known as the
; OTHER INFORMATION: Synthetic scFv library (#1) from the Centre for
; OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3

Query Match          100.0%; Score 576; DB 3; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.3e-47;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SELTOPPAVSVALGQTVRITCGDSLSRYSAWYQKPGQAPVLYIGKNNRPSGIDRF 60
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DB      154 SELTOPPAVSVALGQTVRITCGDSLSRYSAWYQKPGQAPVLYIGKNNRPSGIDRF 213
      |||
QY      61 SSSSGNTASLTITGAQAEDEADYYCNSRPSGSHVFFGGTTLTVLGAA 111
      |||
DB      214 SSSSGNTASLTITGAQAEDEADYYCNSRPSGSHVFFGGTTLTVLGAA 264
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RESULT 2
US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikelsen, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260.527A
; CURRENT FILING DATE: 1999-02-26
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NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 1  
LENGTH: 280  
TYPE: PRT  
ORGANISM: UNKNOWN  
FEATURE:  
OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a  
OTHER INFORMATION: phage display library known as the Synthetic scFv  
OTHER INFORMATION: library (#1) from the Centre for Protein  
OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.  
US-09-260-527-1

Query Match 100.0%; Score 576; DB 3; Length 280;  
Best local Similarity 100.0%; Pred. No. 1.3e-47;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQVTRITCGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 60  
DB 156 SEITDPAVSVALGQVTRITCGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 215  
QY 61 SGSSSGNTASLITTTGAQAEDEADYYCNSRDSGNHVFPGGTRKLTVLGAAA 111  
DB 216 SGSSSGNTASLITTTGAQAEDEADYYCNSRDSGNHVFPGGTRKLTVLGAAA 266

## RESULT 3

US-09-079-029-9  
Sequence 9, Application US/09079029  
Patent No. 6342369  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilla W.  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuntharapai, Anan  
APPLICANT: Kim, Kyung U.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-9

QY 1 SEITDPAVSVALGQVTRITCGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 60  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 176 SEITDPAVSVALGQVTRITCGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 235  
QY 61 SGSSSGNTASLITTTGAQAEDEADYYCNSRDSGNHVFPGGTRKLTVLGAAA 111  
DB 236 SGSSSGNTASLITTTGAQAEDEADYYCNSRDSGNHVFPGGTRKLTVLGAAA 286

## RESULT 4

US-09-079-029-10  
Sequence 10, Application US/09079029  
Patent No. 6342369  
GENERAL INFORMATION:  
APPLICANT: Adams, Camilla W.  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuntharapai, Anan  
APPLICANT: Kim, Kyung U.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,029  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Marschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-10

Query Match 100.0%; Score 576; DB 3; Length 312;  
Best local Similarity 100.0%; Pred. No. 1.5e-47;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQVTRITCGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 60  
DB 179 SEITDPAVSVALGQVTRITCGDLSRSYASWYQKPGQAPLVLYGKNNRPSGIPDRF 238  
QY 61 SGSSSGNTASLITTTGAQAEDEADYYCNSRDSGNHVFPGGTRKLTVLGAAA 111  
DB 239 SGSSSGNTASLITTTGAQAEDEADYYCNSRDSGNHVFPGGTRKLTVLGAAA 289

## RESULT 5

US-09-720-493-4  
Sequence 4, Application US/09720493  
Patent No. 6827925  
GENERAL INFORMATION:  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Williams, Andrew J.  
APPLICANT: Tempest, Philip R.  
APPLICANT: Hollet, Thor L.  
APPLICANT: Main, Sarah H.  
APPLICANT: Jackson, Helen  
APPLICANT: Darmon, Olekan

TITLE OF INVENTION: Improvements relating to antibodies  
FILE REFERENCE: AHB/CP577533  
CURRENT APPLICATION NUMBER: US/09/720,493  
CURRENT FILING DATE: 2002-10-23  
PRIOR APPLICATION NUMBER: GB 9814383.7  
PRIOR FILING DATE: 1998-07-02  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-720-493-4

Query Match 96.9%; Score 558; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 2.3e-46;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTOPPAVSVALGQTVRITCGDLSRSYYASWYQKPGAPVLVIYKNNRPSGIPDRF 60  
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DB 2 SELTOPPAVSVALGQTVRITCGDLSRSYYASWYQKPGAPVLVIYKNNRPSGIPDRF 61  
|||  
QY 61 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGTLTVL 107  
|||  
DB 62 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGTLTVL 108  
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RESULT 6  
US-09-203-768A-8  
Sequence 8, Application US/09203768A  
Patent No. 6787638  
GENERAL INFORMATION:  
APPLICANT: Huse, William D.  
APPLICANT: Mackins, Jeffrey D.  
TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods  
FILE REFERENCE: P-IX 2947  
CURRENT APPLICATION NUMBER: US/09/203,768A  
CURRENT FILING DATE: 1998-12-02  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 111  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-203-768A-8

Query Match 96.2%; Score 554; DB 4; Length 111;  
Best Local Similarity 99.1%; Pred. No. 5.8e-46;  
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SELTOPPAVSVALGQTVRITCGDLSRSYYASWYQKPGAPVLVIYKNNRPSGIPDRF 60  
|||  
DB 2 SELTOPPAVSVALGQTVRITCGDLSRSYYASWYQKPGAPVLVIYKNNRPSGIPDRF 61  
|||  
QY 61 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGTLTVL 108  
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DB 62 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGTLTVL 109  
|||

RESULT 7  
US-08-652-816A-16  
Sequence 16, Application US/08652816A  
Patent No. 5872215  
GENERAL INFORMATION:  
APPLICANT: Osbourn, JK  
APPLICANT: Allen, DJ  
APPLICANT: McGafferty, JG  
TITLE OF INVENTION: Specific binding members, materials and  
TITLE OF INVENTION: methods.  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,816A  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.4  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9125579.8  
FILING DATE: 02-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 23-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9525004.9  
FILING DATE: 07-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9610824.6  
FILING DATE: 23-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02240  
FILING DATE: 02-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/244,597  
FILING DATE: 01-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/33308  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-652-816A-16

Query Match 93.2%; Score 537; DB 2; Length 109;  
Best Local Similarity 96.2%; Pred. No. 2.4e-44;  
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SELTOPPAVSVALGQTVRITCGDLSRSYYASWYQKPGAPVLVIYKNNRPSGIPDRF 60  
|||  
DB 2 SELTOPPAVSVALGQTVRITCGDLSRSYYASWYQKPGAPVLVIYKNNRPSGIPDRF 61  
|||  
QY 61 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGTLTV 106  
|||  
DB 62 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFVGGGTLTV 107  
|||

RESULT 8  
US-08-655-202-34  
Sequence 34, Application US/08655202  
Patent No. 5977322  
GENERAL INFORMATION:  
APPLICANT: Marks, James D.  
APPLICANT: Schier, Robert  
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to  
TITLE OF INVENTION: Tumor Antigens  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/665,202  
FILING DATE: 13-JUN-1996  
CLASSIFICATION: 424  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061410  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-665-202-34  
Query Match 92.3%; Score 531.5; DB 2; Length 109;  
Best Local Similarity 95.4%; Pred. No. 8.1e-44;  
Matches 104; Conservative 2; Mismatches 2; Indels 1; Gaps 1;  
QY 1 SEITDPAVSVALGQTVRTICQGDLSRSYYASWYQKPGQAPVLYIGKNNRPSGIPDRF 60  
DB 1 SEITDPAVSVALGQTVRTICQGDLSRSYYASWYQKPGQAPVLYIGKNNRPSGIPDRF 60  
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGN-HVYFGGTYKLVLG 108  
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGN-HVYFGGTYKLVLG 108  
RESULT 9  
US-09-315-574-34  
Sequence 34, Application US/09315574  
Patent No. 6512097  
GENERAL INFORMATION:  
APPLICANT: Marks, James D.  
APPLICANT: Schier, Robert  
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.  
STREET: Four Embarcadero Center, Suite 1100  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4106  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/315,574  
FILING DATE: 20-MAY-99  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/665,202  
FILING DATE: 13-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061411  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-315-574-34  
Query Match 92.3%; Score 531.5; DB 4; Length 109;  
Best Local Similarity 95.4%; Pred. No. 8.1e-44;  
Matches 104; Conservative 2; Mismatches 2; Indels 1; Gaps 1;  
QY 1 SEITDPAVSVALGQTVRTICQGDLSRSYYASWYQKPGQAPVLYIGKNNRPSGIPDRF 60  
DB 1 SEITDPAVSVALGQTVRTICQGDLSRSYYASWYQKPGQAPVLYIGKNNRPSGIPDRF 60  
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGN-HVYFGGTYKLVLG 108  
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGN-HVYFGGTYKLVLG 108  
RESULT 10  
US-09-726-219A-168  
Sequence 168, Application US/09726219A  
Patent No. 6806079  
GENERAL INFORMATION:  
APPLICANT: Cambridge Antibody Technology  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Medical Research Council  
APPLICANT: McCafferty, John  
APPLICANT: Pope, Anthony  
APPLICANT: Johnson, Kevin  
APPLICANT: Hoogenboom, Hendricus  
APPLICANT: Griffiths, Andrew  
APPLICANT: Jackson, Ronald  
APPLICANT: Holliger, Kasper  
APPLICANT: Marks, James  
APPLICANT: Clarkson, Timothy  
APPLICANT: Chiswell, David  
APPLICANT: Winter, Gregory  
APPLICANT: Bonetti, Timothy  
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
FILE REFERENCE: 213839-00013  
CURRENT APPLICATION NUMBER: US/09/726,219A  
FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: GB 9015198.6  
PRIOR FILING DATE: 1990-07-10  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9024503.6  
PRIOR FILING DATE: 1990-11-12



PRIOR APPLICATION NUMBER: GB 9104744.9  
PRIOR FILING DATE: 1991-03-06  
PRIOR APPLICATION NUMBER: GB 9110549.4  
PRIOR FILING DATE: 1991-05-15  
PRIOR APPLICATION NUMBER: PCT/GB91/01134  
PRIOR FILING DATE: 1991-07-10  
PRIOR APPLICATION NUMBER: US 07/971,857  
PRIOR FILING DATE: 1993-01-08  
PRIOR APPLICATION NUMBER: US 08/484,893  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 168  
LENGTH: 101  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-726-219A-168

Query Match 91.1%; Score 525; DB 4; Length 101;  
Best Local Similarity 100.0%; Pred. No. 3.1e-43;  
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPNPAVSVALGQTVRTTCGDSLSRSTYASWYQKPGAPLVLYGKNNRPSGIPDRF 60  
DB 2 SEITDPNPAVSVALGQTVRTTCGDSLSRSTYASWYQKPGAPLVLYGKNNRPSGIPDRF 61  
QY 61 SGSSSGNTASLTITGAQAEADYDYNCRSDSGNHVFG 100  
DB 62 SGSSSGNTASLTITGAQAEADYDYNCRSDSGNHVFG 101

## RESULT 11

US-08-665-202-35  
Sequence 35, Application US/08665202

PATENT No. 5977322  
GENERAL INFORMATION:  
APPLICANT: Marks, James D.  
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to  
TITLE OF INVENTION: Tumor Antigens  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/665,202  
FILING DATE: 13-JUN-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061410  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 97 amino acids

TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-665-202-35

Query Match 87.2%; Score 502; DB 2; Length 97;  
Best Local Similarity 99.0%; Pred. No. 4.8e-41;  
Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEITDPNPAVSVALGQTVRTTCGDSLSRSTYASWYQKPGAPLVLYGKNNRPSGIPDRF 60  
DB 1 SEITDPNPAVSVALGQTVRTTCGDSLSRSTYASWYQKPGAPLVLYGKNNRPSGIPDRF 60  
QY 61 SGSSSGNTASLTITGAQAEADYDYNCRSDSGNHV 97  
DB 61 SGSSSGNTASLTITGAQAEADYDYNCRSDSGNHV 97

## RESULT 12

US-09-315-574-35  
Sequence 35, Application US/09315574

PATENT No. 6512097  
GENERAL INFORMATION:  
APPLICANT: Marks, James D.  
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to  
TITLE OF INVENTION: Tumor Antigens  
NUMBER OF SEQUENCES: 141  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.  
STREET: Four Embarcadero Center, Suite 1100  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4106  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/315,574  
FILING DATE: 20-MAY-99  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,238  
FILING DATE: 14-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,250  
FILING DATE: 15-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 02307E-061411  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 97 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-315-574-35

Query Match 87.2%; Score 502; DB 4; Length 97;  
Best Local Similarity 99.0%; Pred. No. 4.8e-41;  
Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SELTODPAVSVALGQTVRITCOGDSLRSYASWYQKPGQAPVLYIGKNNRPSGIPDRF 60  
Db 1 SSILOPAPVSVAGQTVRITCOGDSLRSYASWYQKPGQAPVLYIGKNNRPSGIPDRF 60  
QY 61 SGSSSGNTASLITGAQAEDEADYCNRSRDSGNHVV 97  
Db 61 SGSSSGNTASLITGAQAEDEADYCNRSRDSGNHVV 97

RESULT 13  
US-08-793-450-2  
; Sequence 2, Application US/08793450  
; Patent No. 6312690  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: MARGARITTE, CHRISTEL  
; APPLICANT: KACZOREK, MICHEL  
; APPLICANT: CHABIBI, HASSAN  
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,450  
; FILING DATE: 03-MAR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94/10566  
; FILING DATE: 02-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 104 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-793-450-2

Query Match 85.9%; Score 494.5; DB 3; Length 104;  
Best Local Similarity 90.7%; Pred. No. 2,7e-40;  
Matches 97; Conservative 2; Mismatches 3; Indels 5; Gaps 1;  
QY 2 ELTODPAVSVALGQTVRITCOGDSLRSYASWYQKPGQAPVLYIGKNNRPSGIPDRF 61  
Db 3 ELTODPAVSVALGQTVRITCOGDSLRSYASWYQKPGQAPVLYIGKNNRPSGIPDRF 62  
QY 62 SGSSSGNTASLITGAQAEDEADYCNRSRDSGNHVVFGGKTLTVLG 108  
Db 63 SGSSSGNTASLITGAQAEDEADYCNRSRDSGNHVVFGGKTLTVLG 104

RESULT 14  
US-08-793-450-6  
; Sequence 6, Application US/08793450

; Patent No. 6312690  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: MARGARITTE, CHRISTEL  
; APPLICANT: KACZOREK, MICHEL  
; APPLICANT: CHABIBI, HASSAN  
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,450  
; FILING DATE: 03-MAR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94/10566  
; FILING DATE: 02-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 238 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-793-450-6

Query Match 85.9%; Score 494.5; DB 3; Length 238;  
Best Local Similarity 90.7%; Pred. No. 6.9e-40;  
Matches 97; Conservative 2; Mismatches 3; Indels 5; Gaps 1;  
QY 2 ELTODPAVSVALGQTVRITCOGDSLRSYASWYQKPGQAPVLYIGKNNRPSGIPDRF 61  
Db 22 ELTODPAVSVALGQTVRITCOGDSLRSYASWYQKPGQAPVLYIGKNNRPSGIPDRF 81  
QY 62 SGSSSGNTASLITGAQAEDEADYCNRSRDSGNHVVFGGKTLTVLG 108  
Db 82 SGSSSGNTASLITGAQAEDEADYCNRSRDSGNHVVFGGKTLTVLG 123

RESULT 15  
US-09-240-274-49  
; Sequence 49, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; CURRENT FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 49  
LENGTH: 104  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: anti-Rh(D) chain J04  
US-09-240-274-49

Query Match 84.5%; Score 487; DB 3; Length 104;  
Best Local Similarity 92.2%; Pred. No. 1,4e-39;  
Matches 95; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 5 QDPVAVVVALGQTVRTICQGDLSRSYYASWTQOKPGQAPLVIVYKNNRPSGIPDRFSGSS 64  
DB 4 QDPVAVVVALGQTVRTICQGDLSRSYYASWTQOKPGQAPLVIVYKNNRPSGIPDRFSGSS 63  
QY 65 SGN TASLITITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVL 107  
DB 64 SGN TASLITITGAQAEDEADYYCSSRGSP--HVAFGGGTKLTVL 104

Search completed: April 25, 2005, 21:12:10  
Job time : 18.1053 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: April 25, 2005, 19:56:06 ; Search time 68.0521 Seconds  
(without alignments)  
630.846 Million cell updates/sec

Title: US-10-029-926d-7  
Perfect score: 576  
Sequence: 1 SEITQDPAAVVALGQTVRLT.....SGNHVFGGKTLVLGAAA 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	576	100.0	111	5	ABG78132 Human Fv
2	576	100.0	111	5	ABG91823 Human ant
3	576	100.0	112	8	ADJ57867 Common li
4	576	100.0	209	5	AAU98017 Human ace
5	576	100.0	249	8	ADR23324 Human CD7
6	576	100.0	260	5	ABG92023 Antibody
7	576	100.0	263	5	ABG92024 Antibody
8	576	100.0	266	5	ABG92020 Human ant
9	576	100.0	277	5	ABG78150 Human Fv
10	576	100.0	277	5	ABG78328 Human Fv
11	576	100.0	277	5	ABG92019 Human ant
12	576	100.0	277	5	ABG91841 Human ant
13	576	100.0	277	8	ADJ28366 Human scf
14	576	100.0	278	8	ADJ28367 Human scf
15	576	100.0	280	4	AAE02186 PAM2 sing
16	576	100.0	280	8	ADJ28368 Human scf
17	576	100.0	280	8	ADJ57363 P-selecti
18	576	100.0	282	4	AAE02185 PAM1 sing
19	576	100.0	309	2	AAW83322 Single ch
20	576	100.0	309	5	ABW09603 Amino aci
21	576	100.0	309	6	ABG74384 Single ch
22	576	100.0	309	7	ADG96737 Human sin
23	576	100.0	309	8	ADG40446 Human sin
24	576	100.0	312	2	AAW83323 Single ch
25	576	100.0	312	5	ABW09604 Amino aci

## ALIGNMENTS

26	576	100.0	312	6	ABG74385	Abg74385 Single ch
27	576	100.0	312	7	ADG98738	Adg98738 Human sin
28	576	100.0	312	8	ADG40447	Adg40447 Human sin
29	570	99.0	274	8	ADG25153	Adg25153 Melanoma
30	568	98.6	110	8	ADG12488	Adg12488 Human IGF
31	568	98.6	110	8	ADG12484	Adg12484 Human IGF
32	568	98.6	215	8	ADR23362	Adr23362 Human CD7
33	565	98.1	229	2	AAW49694	Aaw49694 Human scf
34	565	98.1	254	2	AAW49693	Aaw49693 Human scf
35	564	97.9	108	4	AAW62939	Aaw62939 Amino aci
36	564	97.9	108	5	AAW80198	Aaw80198 Human gp9
37	564	97.9	109	4	AAU02513	Aau02513 Ant1-adip
38	564	97.9	236	2	AAW49690	Aaw49690 Human scf
39	564	97.9	237	2	AAW49691	Aaw49691 Human Bly
40	564	97.9	237	5	ABP46101	Abp46101 Human Bly
41	564	97.9	237	5	ABP45930	Abp45930 Human Bly
42	564	97.9	237	7	ADG96928	Adg96928 Single ch
43	564	97.9	237	7	ADG96757	Adg96757 Single ch
44	564	97.9	238	5	ABP45896	Abp45896 Human Bly
45	564	97.9	238	7	ADG96723	Adg96723 Single ch

RESULT 1  
ABG78132  
ID ABG78132 standard; protein; 111 AA.

AC ABG78132;  
DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #7.

XX Human Fv molecule; hypervariable region; single chain Fv; cytostatic;  
XX disulfide Fv; defv; scfv; cancer; carcinoma; sarcoma; leukemia; adenoma;  
XX lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukemia.

OS Homo sapiens.

PN WO200259264-A2.

PD 01-AUG-2002.

PF 31-DEC-2001; 2001WO-US049440.

PR 29-DEC-2000; 2000US-00751181.

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Lavanon A;  
XX Plakshin D, Peretz T;

XX WPI; 2002-619166/66.

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
PT or fragment, or construct of fragment with enhanced binding  
PT characteristics so as to selectively bind target cell in favor of other  
PT cells.

PS Disclosure; Page 150; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv  
XX molecule, a construct or fragments or a construct of a fragment with  
XX enhanced binding characteristics which selectively and/or specifically  
XX binds to a target cell in favour of other cells, where binding is  
XX primarily determined by a first hypervariable region and Fv is a single  
XX chain Fv (scfv) or a disulfide Fv (dsfv). The peptide, optionally in  
XX association with or attached, coupled, linked or fused to a  
XX pharmaceutical agent, is useful in the manufacture of a medicament, where  
XX the medicament has actively against a diseased cell, preferably a cancer  
XX cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,

CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention

CC Sequence 111 AA;

Query Match 100.0%; Score 576; DB 5; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-35;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIPDRF 60

DB 1 SEITDPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIPDRF 60

QY 61 SSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFPGGITLVLGAAA 111

DB 61 SSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFPGGITLVLGAAA 111

#### RESULT 2

ABG91823 standard; protein; 111 AA.

ABG91823;

04-DEC-2002 (first entry)

Human antibody fragment #7.

Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;  
 KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
 KM myocardial infarction; retinopathic disease; abnormal platelet function;  
 KM sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.

PN WO200253700-A2.

PD 11-JUL-2002.

PF 31-DEC-2001; 2001WO-US049442.

PR 29-DEC-2000; 2000US-00751181.

PR 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
 PI Sthanon E, Richter T, Amit B, Koopman L, Peretz T, Levanon A;

XX WPI; 2002-674776/72.

Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer.

XX Disclosure; Page 227-228; 0pp; English.

XX The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility

CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia  
 CC cells in a patient, or in the manufacture of a medicament for the above  
 CC mentioned purposes. The epitopes are useful for diagnosing and treating  
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
 CC diseases, cardiovascular diseases such as myocardial infarction,  
 CC retinopathic diseases and other diseases mediated by abnormal platelet  
 CC function and diseases caused by sulphated tyrosine-dependent protein-  
 CC protein interactions. This sequence represents a human antibody fragment  
 CC of the invention

XX Sequence 111 AA;

Query Match 100.0%; Score 576; DB 5; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-35;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIPDRF 60

DB 1 SEITDPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIPDRF 60

QY 61 SSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFPGGITLVLGAAA 111

DB 61 SSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFPGGITLVLGAAA 111

#### RESULT 3

ADJ57867 standard; protein; 112 AA.

ADJ57867;

06-MAY-2004 (first entry)

Common light variable chain protein of B29, II-2 and I-2.

XX Cytostatic; immunosuppressive; Antibacterial; Virucide; Fungicide;  
 KM Antiparasitic; auto-immune disease; cancer; neoplastic disorder;  
 KM leukemia.

OS Synthetic.

PN WO2004009618-A2.

PD 29-JAN-2004.

PF 15-JUL-2003; 2003WO-EP007690.

PR 18-JUL-2002; 2002EP-00077953.

PR 18-JUL-2002; 2002US-0397066P.

PR 27-MAY-2003; 2003WO-EP050201.

XX (CRUC-) CRUCELL HOLLAND BV.

PI Van Berkel PHC, Brus RHP, Bout A, Logtenberg T;

XX WPI; 2004-132914/13.

DR N-PSDB; ADJ57866.

XX Producing mixture of antibodies in recombinant host comprises expressing  
 PT nucleic acid sequence(s) encoding light chain and three different heavy  
 PT chains capable of pairing with light chain in recombinant host cell.

XX Disclosure; SEQ ID NO 18; 186pp; English.

XX The present invention relates to producing a mixture of antibodies in a  
 CC recombinant host comprises expressing in a recombinant host cell a  
 CC nucleic acid sequence or nucleic acid sequences encoding a light chain  
 CC and at least three different heavy chains that are capable of pairing  
 CC with a light chain. The method is useful for producing a mixture of  
 CC antibodies in a recombinant host, is useful for the preparation of a  
 CC medicament for use in the treatment or diagnosis of a disease or disorder  
 CC in a human or animal. The antibodies are useful for treating auto-immune

CC disease and cancer such as solid tumors of the brain, head and neck,  
 CC breast, prostate, colon, lung, etc.; hematologic tumors such as B-cell  
 CC tumors, neoplastic disorders such as leukemia, lymphoma, sarcoma,  
 CC carcinoma, neural cell tumors, myelomas, melanomas, neuroblastomas, etc.,  
 CC and are also useful for treating graft-versus-host rejections, infectious  
 CC diseases due to pathogenic bacteria such as multidrug resistant  
 CC *Staphylococcus aureus*, fungi such as *Candida albicans*, as prophylaxis  
 CC against viruses such as rabies virus, for treating or preventing disease  
 CC caused by adenoviruses, respiratory syncytium virus, and for treating  
 CC diseases caused by unicellular or multicellular parasites. The method  
 CC enables exploring many combinations simultaneously, where the  
 CC combinations include the presence of bispecific antibodies in the  
 CC produced mixture. The present sequence represents the common light  
 CC variable chain of B28, II-2 and I-2.

XX  
 SQ Sequence 112 AA;  
 Query Match 100.0%; Score 576; DB 8; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-35;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSAVGQTVRITCGDLSRSYYASWYQKPGQAPLVITYGKNNRPSGIPDRF 60  
 DB 2 SEITDPAVSAVGQTVRITCGDLSRSYYASWYQKPGQAPLVITYGKNNRPSGIPDRF 61  
 QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRPSGNNHVFEGGKTLTVGAAA 111  
 DB 62 SSSSGNTASLTITGAQAEDEADYYCNSRPSGNNHVFEGGKTLTVGAAA 112

RESULT 4  
 AAU98017  
 ID AAU98017 standard; protein; 209 AA.  
 AC AAU98017;  
 DT 27-AUG-2002 (first entry)  
 XX  
 XX Human acetylcholinesterase antibody PD-antibasp 1.  
 DE  
 XX  
 KW Human; synaptic acetylcholinesterase; PD-antibasp 1; antibody;  
 KW single-chain variable region; scFv; AChE-S;  
 KW heavy chain variable region; progressive neuromuscular disorder;  
 KW muscle distortion; muscle re-innervation; myasthenia gravis;  
 KW neuromuscular junction abnormality; Eaton-Lambert disease;  
 KW muscular dystrophy; amyotrophic lateral sclerosis; ALS;  
 KW post-traumatic stress disorder; PTSD; multiple sclerosis; Dystonia;  
 KW post-stroke scleriosis; post-injury muscle damage;  
 KW excessive re-innervation.  
 KM  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200246422-A1.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 22-MAY-2001; 2001WO-IL000464.  
 XX  
 PR 04-DEC-2000; 2000IL-00140071.  
 XX  
 PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 XX  
 PI Soreq H, Flores CF, Nissim A;  
 XX  
 DR WPI; 2002-463832/49.  
 DR N-PSDB; ABK52915.  
 XX  
 PT Nucleic acid sequence coding for a single-chain variable fragment (scFv)  
 PT antibody that has specific affinity for the synaptic variant of  
 PT acetylcholinesterase (AChE-S), useful for diagnosing a neuromuscular  
 PT disorder, e.g. Myasthenia gravis.  
 XX  
 PS Claim 11; Page 61-63; 73pp; English.

XX  
 CC The invention relates to a nucleic acid sequence coding for a single-  
 CC chain variable fragment (scFv) antibody that has specific affinity for  
 CC the synaptic variant of acetylcholinesterase (AChE-S), where the scFv  
 CC antibody consists essentially of a polypeptide comprising the binding  
 CC portion of the heavy chain variable region of an antibody. Also included  
 CC are an expression vehicle comprising a nucleic acid sequence coding for a  
 CC scFv antibody that has specific affinity for the synaptic variant of AChE  
 CC -S, an scFv antibody specifically recognising and binding to the synaptic  
 CC variant of AChE-S and a method for the diagnosis of a progressive  
 CC neuromuscular disorder in a mammal, comprising obtaining a sample from  
 CC the mammal and detecting intensified expression of at least one of the  
 CC AChE variants in the sample. The single-chain Fv antibody is useful for  
 CC diagnosing a progressive neuromuscular disorder which involves any one of  
 CC muscle distortion, muscle re-innervation and neuromuscular junction (NMJ)  
 CC abnormalities. The disorder is Myasthenia gravis (preferred), Eaton-  
 CC Lambert disease, muscular dystrophy, amyotrophic lateral sclerosis (ALS),  
 CC post-traumatic stress disorder (PTSD), multiple sclerosis, Dystonia, post  
 CC -stroke scleriosis, post-injury muscle damage, excessive re-innervation,  
 CC or post-exposure to AChE inhibitors. The present sequence represents an  
 CC anti-AChE scFv antibody, PD-antibasp 1

XX  
 SQ Sequence 209 AA;  
 Query Match 100.0%; Score 576; DB 5; Length 209;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-35;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSAVGQTVRITCGDLSRSYYASWYQKPGQAPLVITYGKNNRPSGIPDRF 60  
 DB 76 SEITDPAVSAVGQTVRITCGDLSRSYYASWYQKPGQAPLVITYGKNNRPSGIPDRF 135  
 QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRPSGNNHVFEGGKTLTVGAAA 111  
 DB 136 SSSSGNTASLTITGAQAEDEADYYCNSRPSGNNHVFEGGKTLTVGAAA 186

RESULT 5  
 ADR23324  
 ID ADR23324 standard; protein; 249 AA.  
 XX  
 AC ADR23324;  
 XX  
 DT 04-NOV-2004 (first entry)  
 XX  
 DE Human CD72-targeted scFv Sc02-025.  
 XX  
 KW Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;  
 KW immunosuppressive; cancer; autoimmune disease; gene therapy.  
 KM  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 101..112  
 FT /label= CDR3  
 XX  
 PN WO2004067569-A1.  
 XX  
 PD 12-AUG-2004.  
 XX  
 PF 27-JAN-2003; 2003WO-EP050004.  
 XX  
 PR 27-JAN-2003; 2003WO-EP050004.  
 XX  
 PA (CRUC-) CRUCCELL HOLLAND BV.  
 XX  
 PI Bakker ABH, Marijssen WB;  
 XX  
 DR WPI; 2004-580978/56.  
 DR N-PSDB; ADR23323.  
 XX  
 PT New internalizing human binding molecules capable of specifically binding  
 PT to CD72, useful for diagnosing and/or treating B-cell associated

PT diseases, such as cancer or autoimmune disorders.

XX Example 3; SEQ ID NO 16; 174pp; English.

XX The present sequence is the protein sequence of SC02-025, an scFv that  
CC specifically recognises human B cell associated antigen CD72. It  
CC comprises V<sub>H</sub>1 DP07 and V<sub>H</sub>1 germline sequences. The scFv was selected  
CC from an antibody phage display library using human tonsillar mononuclear  
CC cells as target. It was shown to selectively bind to peripheral blood  
CC CD19<sup>+</sup> B cells and to CD72-transfected U937 cells. Plasmid DNA was  
CC obtained from the scFv clone and used to determine the scFv nucleic acid  
CC and amino acid sequences. SC02-025 scFv was used to generate CD72-  
CC directed human IgG1 antibodies comprising heavy chain ADR23350 and light  
CC chain ADR23362 sequences. Such anti-CD72 immunoglobulins or their antigen  
CC binding fragments can be used as internalising human binding molecules  
CC of the invention. These internalising human binding molecules are capable  
CC of (specifically) binding to CD72 or its antigenic determinant, and  
CC present on the surface of target cells. Upon binding to CD72  
CC internalise. In addition to the internalising human binding molecules,  
CC the invention provides immunoconjugates comprising an internalising human  
CC binding molecule and a tag (toxic substance, radioactive substance,  
CC liposome and/or enzyme), nucleic acids encoding these, and compositions  
CC comprising them. The internalising human binding molecule,  
CC immunoconjugate, nucleic acid molecule or composition can be used in the  
CC diagnosis and/or treatment of a B cell associated disorder or disease,  
CC especially a B cell associated cancer and B cell associated autoimmune  
CC disorder (claimed).

XX Sequence 249 AA;

XX Query Match 100.0%; Score 576; DB 8; Length 249;  
XX Best Local Similarity 100.0%; Pred. No. 6.2e-35;  
XX Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLYYGNRRSGIPDRF 60  
DB 139 SEITDPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLYYGNRRSGIPDRF 198  
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTGLTVLGAAA 111  
DB 199 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTGLTVLGAAA 249

RESULT 6

ID ABG92023 standard; protein; 260 AA.

XX ABG92023;

DT 04-DEC-2002 (first entry)

XX Antibody protein #3.

DE Antibody; epitope; cancer; tumour; cell rolling; inflammation;

XX metastasis; hypervariable region; autoimmune disease; thrombosis;

KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;

KW myocardial infarction; retinopathic disease; abnormal platelet function;

KW sulphated tyrosine-dependent protein-protein interaction.

XX Unidentified.

OS WO200253700-A2.

XX 11-JUL-2002.

XX 31-DEC-2001; 2001WO-US049442.

XX 29-DEC-2000; 2000US-00751181.

XX 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX

PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H,  
PI Sznathon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;  
XX WPI; 2002-674776/72.

PT Novel isolated epitope present on cancer cells and important in  
PT physiological phenomena such as cell rolling, metastasis and  
PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
PT diseases, and cancer.

PS Disclosure; Fig 49; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and  
CC important in physiological phenomena such as cell rolling, metastasis and  
CC inflammation, where the epitope is capable of being bound by an antibody,  
CC its antigen-binding fragment or its complex comprising at least one  
CC antibody or its binding fragment having a first hypervariable region. The  
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
CC mortality of tumour or leukaemia cells, for increasing the susceptibility  
CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
CC leukaemia agents, or for decreasing the number of tumour or leukaemia  
CC cells in a patient, or in the manufacture of a medicament for the above  
CC mentioned purposes. The epitopes are useful for diagnosing and treating  
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
CC diseases, cardiovascular diseases such as myocardial infarction,  
CC retinopathic diseases and other diseases mediated by abnormal platelet  
CC function and diseases caused by sulphated tyrosine-dependent protein-  
CC protein interactions. This sequence represents an antibody protein of the  
CC invention

XX Sequence 260 AA;

XX Query Match 100.0%; Score 576; DB 5; Length 260;  
XX Best Local Similarity 100.0%; Pred. No. 6.5e-35;  
XX Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLYYGNRRSGIPDRF 60  
DB 136 SEITDPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLYYGNRRSGIPDRF 195  
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTGLTVLGAAA 111  
DB 196 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFFGGTGLTVLGAAA 246

RESULT 7

ID ABG92024 standard; protein; 263 AA.

XX ABG92024;

DT 04-DEC-2002 (first entry)

XX Antibody protein #4.

DE Antibody; epitope; cancer; tumour; cell rolling; inflammation;

XX metastasis; hypervariable region; autoimmune disease; thrombosis;

KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;

KW myocardial infarction; retinopathic disease; abnormal platelet function;

KW sulphated tyrosine-dependent protein-protein interaction.

XX Unidentified.

OS WO200253700-A2.

XX 11-JUL-2002.

XX 31-DEC-2001; 2001WO-US049442.

XX



PR 29-DEC-2000; 2000US-00751181.  
 PR 29-DEC-2000; 2000US-0258948P.  
 XX  
 XX  
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 PI Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;  
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;  
 XX  
 XX WPI; 2002-674776/72.  
 DR  
 XX  
 PT Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer.  
 XX  
 PS Disclosure; Fig 50; Opp; English.  
 XX  
 CC The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility  
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia  
 CC cells in a patient, or in the manufacture of a medicament for the above  
 CC mentioned purposes. The epitopes are useful for diagnosing and treating  
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
 CC diseases, cardiovascular diseases such as myocardial infarction,  
 CC retinopathic diseases and other diseases mediated by abnormal platelet  
 CC function and diseases caused by sulphated tyrosine-dependent protein-  
 CC protein interactions. This sequence represents an antibody protein of the  
 CC invention  
 CC  
 SQ Sequence 263 AA;  
 XX  
 Query Match 100.0%; Score 576; DB 5; Length 263;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-35;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEITDPAVSVALGQTVRITTCGDSLSRYSYASWYQKPGAPLVLYGKNNRPSGIPDRF 60  
 DB 133 SEITDPAVSVALGQTVRITTCGDSLSRYSYASWYQKPGAPLVLYGKNNRPSGIPDRF 192  
 QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGCTKLTVLGAAA 111  
 DB 193 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGCTKLTVLGAAA 243

RESULT 8  
 ABG92020  
 ID ABG92020 standard; protein; 266 AA.  
 AC  
 XX ABG92020;  
 DT 04-DEC-2002 (first entry)  
 XX  
 DE Human antibody fragment #204.  
 XX  
 XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;  
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
 KW myocardial infarction; retinopathic disease; abnormal platelet function;  
 KW sulphated tyrosine-dependent protein-protein interaction.  
 OS Homo sapiens.  
 XX  
 XX  
 PN MO200253700-A2.

XX  
 PD 11-JUL-2002.  
 XX  
 PF 31-DEC-2001; 2001WO-US049442.  
 XX  
 XX  
 PR 29-DEC-2000; 2000US-00751181.  
 PR 29-DEC-2000; 2000US-0258948P.  
 XX  
 XX  
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 PI Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;  
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;  
 XX  
 XX WPI; 2002-674776/72.  
 DR  
 XX  
 PT Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer.  
 XX  
 PS Disclosure; Page 309-310; Opp; English.  
 XX  
 CC The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility  
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia  
 CC cells in a patient, or in the manufacture of a medicament for the above  
 CC mentioned purposes. The epitopes are useful for diagnosing and treating  
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
 CC diseases, cardiovascular diseases such as myocardial infarction,  
 CC retinopathic diseases and other diseases mediated by abnormal platelet  
 CC function and diseases caused by sulphated tyrosine-dependent protein-  
 CC protein interactions. This sequence represents a human antibody fragment  
 CC of the invention  
 CC  
 SQ Sequence 266 AA;  
 XX  
 Query Match 100.0%; Score 576; DB 5; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-35;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SEITDPAVSVALGQTVRITTCGDSLSRYSYASWYQKPGAPLVLYGKNNRPSGIPDRF 60  
 DB 153 SEITDPAVSVALGQTVRITTCGDSLSRYSYASWYQKPGAPLVLYGKNNRPSGIPDRF 212  
 QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGCTKLTVLGAAA 111  
 DB 213 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGCTKLTVLGAAA 263

RESULT 9  
 ABG78150  
 ID ABG78150 standard; protein; 277 AA.  
 AC  
 XX ABG78150;  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Human Fv molecule hypervariable region related peptide #25.  
 XX  
 XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;  
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.  
 XX

OS Homo sapiens.  
 XX WO200259264-A2.  
 PN 01-AUG-2002.  
 XX 31-DEC-2001; 2001WO-US049440.  
 XX 29-DEC-2000; 2000US-00751181.  
 XX (BIOI-) BIO-TECHNOLOGY GEN CORP.  
 PA Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;  
 PI Plakein D, Peretz T;  
 XX WPI; 2002-619166/66.  
 DR Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 XX or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favor of other  
 PT cells.  
 PS Claim 4; Page 155-156; 232pp; English.  
 XX The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments of a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention  
 CC  
 XX SQ Sequence 277 AA;  
 Query Match 100.0%; Score 576; DB 5; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-35;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SELTDPAVSVALGQTVRITCGDLSRSYASWYQKPGAPVLVIYGNRRPSGIPDRF 60  
 Db 153 SELTDPAVSVALGQTVRITCGDLSRSYASWYQKPGAPVLVIYGNRRPSGIPDRF 212  
 QY 61 SSSSSGNTASLTITGAQAEDEADYCNRRDSSGNHVFPGGTYLTVLGAAA 111  
 Db 213 SSSSSGNTASLTITGAQAEDEADYCNRRDSSGNHVFPGGTYLTVLGAAA 263

RESULT 10  
 ABG78328  
 ID ABG78328 standard; protein; 277 AA.  
 XX ABG78328;  
 AC  
 XX 15-NOV-2002 (first entry)  
 DT  
 XX Human Fv molecule hypervariable region related peptide #203.  
 DE Human Fv molecule hypervariable region; single chain Fv; cytosolic;  
 XX Human; Fv molecule; hypervariable region; single chain Fv; cytosolic;  
 KW disulfide Fv; dsFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200259264-A2.  
 PN  
 XX

PD 01-AUG-2002.  
 XX 31-DEC-2001; 2001WO-US049440.  
 PF 29-DEC-2000; 2000US-00751181.  
 XX (BIOI-) BIO-TECHNOLOGY GEN CORP.  
 PA Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;  
 PI Plakein D, Peretz T;  
 XX WPI; 2002-619166/66.  
 DR N-PSDB; ABS63384.  
 DR Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 XX or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favor of other  
 PT cells.  
 PS Claim 14; Fig 14; 232pp; English.  
 XX The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments of a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention  
 CC  
 XX SQ Sequence 277 AA;  
 Query Match 100.0%; Score 576; DB 5; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-35;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SELTDPAVSVALGQTVRITCGDLSRSYASWYQKPGAPVLVIYGNRRPSGIPDRF 60  
 Db 153 SELTDPAVSVALGQTVRITCGDLSRSYASWYQKPGAPVLVIYGNRRPSGIPDRF 212  
 QY 61 SSSSSGNTASLTITGAQAEDEADYCNRRDSSGNHVFPGGTYLTVLGAAA 111  
 Db 213 SSSSSGNTASLTITGAQAEDEADYCNRRDSSGNHVFPGGTYLTVLGAAA 263

RESULT 11  
 ABG92019  
 ID ABG92019 standard; protein; 277 AA.  
 XX ABG92019;  
 AC  
 XX 04-DEC-2002 (first entry)  
 DT  
 XX Human antibody fragment #203.  
 DE Human antibody fragment #203.  
 XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;  
 KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
 KW myocardial infarction; retinopathy disease; abnormal platelet function;  
 KM sulphated tyrosine-dependent protein-protein interaction.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200253700-A2.  
 PN  
 XX 11-JUL-2002.  
 PD

XX	31-DEC-2001; 2001WO-US049442.
PP	
XX	29-DEC-2000; 2000US-00751181.
FR	29-DEC-2000; 2000US-0258948P.
PR	
XX	(BIOT-) BIO-TECHNOLOGY GEN CORP.
PA	Lazarovits J, Hagai Y, Plaksein D, Vogel T, Nimrod A, Mer-Haim H;
PI	Szantonon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
P1	WPI, 2002-674776/72.
XX	
DR	
XX	
PT	Novel isolated epitope present on cancer cells and important in
FT	physiological phenomena such as cell rolling, metastasis and
PT	inflammation, for treating autoimmune, inflammatory or cardiovascular
XX	diseases, and cancer.
PS	Claim 23; Page 308-309; Opp: English.
XX	
CC	The invention relates to an isolated epitope present on cancer cells and
CC	important in physiological phenomena such as cell rolling, metastasis and
CC	inflammation, where the epitope is capable of being bound by an antibody,
CC	its antigen-binding fragment or its complex comprising at least one
CC	antibody or its binding fragment having a first hypervariable region. The
CC	epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC	diseases, thrombosis, reasthenosis, metastasis, growth and/or replication of
CC	tumour or leukaemia cells, increase in number of tumour or leukaemia
CC	cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC	platelet and/or cell-platelet adhesion or aggregation, for increasing
CC	mortality of tumour or leukaemia cells, for increasing the susceptibility
CC	of diseased cells to damage by anti-disease, anti-cancer or anti-
CC	leukaemia agents, or for decreasing the number of tumour or leukaemia
CC	cells in a patient, or in the manufacture of a medicament for the above
CC	mentioned purposes. The epitopes are useful for diagnosing and treating
CC	diseases such as cancer, leukemia, autoimmune diseases, inflammatory
CC	diseases, cardiovascular diseases such as myocardial infarction,
CC	retinopathic diseases and other diseases mediated by abnormal platelet
CC	function and diseases caused by sulphated tyrosine-dependent protein-
CC	protein interactions. This sequence represents a human antibody fragment
CC	of the invention
XX	
SO	Sequence 277 AA;
	Query Match                      100.0%; Score 576; DB 5; Length 277;
	Best Local Similarity        100.0%; Pred. No. 6.9e-35;
	Matches    111; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
OY	1 SELTODPAVSVALGQTVRITCGDSLRSVYSWYOQKFGAPVLVIYKNNRPSPGIDPRF 60
DB	153 SELTODPAVSVALGQTVRITCGDLSRSVYSWSYQKFGAPVLVIYCKNRRPSPGIDPRF 212
OY	61 SGSSSGNNASTLTTCGAQAEDEADYYCNSRDSSGNHVVGGGTKLTVLGAAA 111
DB	213 SGSSSGNNASTLTTCGAQAEDEADYYCNSRDSSGNHVVGGGTKLTVLGAAA 263
ID	ABG91841 standard; proteicn; 277 AA.
AC	ABG91841;
XX	
DT	04-DEC-2002 (first entry)
XX	
DE	Human antibody fragment #25.
XX	
KW	Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW	metastasis; hypervariable region; autoimmune disease; thrombosis;
KW	reastenosis; leukemia; inflammatory disease; cardiovascular disease;
KW	myocardial infarction; retinopathic disease; abnormal platelet function;
XX	sulphated tyrosine-dependent protein-protein interaction.

OS	Homo sapiens.
XX	WO200253700-A2.
XX	11-JUL-2002.
XX	31-DEC-2001; 2001WO-US049442.
XX	29-DEC-2000; 2000US-00751181.
XX	PR 29-DEC-2000; 2000US-0258948P.
XX	(BIOT-) BIO-TECHNOLOGY GEN CORP.
XX	Lazarovite J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H,
PI	Szantonon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX	WPI; 2002-674776/72.
DR	
XX	Novel isolated epitope present on cancer cells and important in
PT	physiological phenomena such as cell rolling, metastasis and
PT	inflammation, for treating autoimmune, inflammatory or cardiovascular
PT	diseases, and cancer.
PS	Claim 23; Page 233-234; Opp; English.
XX	The invention relates to an isolated epitope present on cancer cells and
CC	important in physiological phenomena such as cell rolling, metastasis and
CC	inflammation, where the epitope is capable of being bound by an antibody,
CC	its antigen-binding fragment or its complex comprising at least one
CC	antibody or its binding fragment having a first hypervariable region. The
CC	epitopes are useful for inhibiting cell rolling. Inflammation, autoimmune
CC	diseases, thrombosis, restenosis, metastasis, growth and/or replication of
CC	tumour or leukaemia cells, increase in number of tumour or leukaemia
CC	cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC	platelet and/or cell-platelet adhesion or aggregation, for increasing
CC	mortality of tumour or leukaemia cells, for increasing the susceptibility
CC	of diseased cells to damage by anti-disease, anti-cancer or anti-
CC	leukaemia agents, or for decreasing the number of tumour or leukaemia
CC	cells in a patient, or in the manufacture of a medicament for the above
CC	mentioned purposes. The epitopes are useful for diagnosing and treating
CC	diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC	diseases, cardiovascular diseases such as myocardial infarction,
CC	retinopathic diseases and other diseases mediated by abnormal platelet
CC	function and diseases caused by sulphated tyrosine-dependent protein-
CC	protein interactions. This sequence represents a human antibody fragment
CC	of the invention
SO	Sequence 277 AA:
	Query Match                      100.0%; Score 576; DB 5; Length 277;
	Best Local Similarity    100.0%; Pred. No. 6.9e-35;
	Matches    111; Conservative    0; Mismatches    0; Indels     0; Gaps     0
OY	1 SELTODPAVSVALGCTVITTCGGDSLRSYASWYOOKRGQAFVLVIYGKNNRPSGIPDRF 60
DB	153 SELTODPAVSVALGCTVITTCGGSLRSYASWYOOKRGQAFLVLIYGKNNRPSGIPDRF 212
OY	61 SGSSSGNASTLTITGAOAEADADYYCNSRDSSGNHVVGGRKLTVLGAA 111
DB	213 SGSSSGNASTLTITGAOAEADADYYCNSRDSSGHNVHVGGRKLTIVLGA 263
 RESULT 13 ADI28366 ADI28366 standard; protein; 277 AA.  ADI28366;  06-MAY-2004 (first entry)  Human scFv fragment Y1, binds to platelets.  Human; antibody; scFv; platelet; drug delivery; cancer; therapy.	

XX Homo sapiens.  
OS  
XX MO2004002528-A1.  
XX  
XX 08-JAN-2004.  
XX  
XX 30-JUN-2003; 2003MO-US020604.  
XX  
XX 01-JUL-2002; 2002US-00189025.  
XX  
XX (SAVI-) SAVIENT PHARM INC.  
XX  
XX Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;  
XX WPI; 2004-099189/10.  
XX  
XX Composition comprising an agent and/or antibody or its fragment, useful  
XX for treating auto-immune disease, thrombosis, restenosis, metastasis, or  
XX PT for inhibiting growth and/or replication of tumor cells or leukemia  
XX cells.  
XX  
XX Claim 13; SEQ ID NO 1; 58pp; English.  
XX  
XX The present sequence is the protein sequence of human scfv fragment Y1.  
XX This antibody was identified by screening a human antibody phage library  
XX that has diversity only in the heavy chain CDR3 regions. Fixed human  
XX platelets were screened in order to identify antibodies that bind  
XX platelets. The epitope for Y1 antibody is located between amino acids 272  
XX and 285 on glycosylated, a subunit of the CD42 complex. Y1 also binds the  
XX C-terminal of PEG-1, a receptor for E-, L- and P-selectin, and has a  
XX high affinity for primary leukemia cells. The invention relates to  
XX compositions utilising an agent and an antibody or its fragment. The  
XX agent is a toxin, radioisotope or pharmaceutical agent such as  
XX doxorubicin. It is complexed or combined with or conjugated to the  
XX antibody or its fragment. The agent and/or antibody can be present in the  
XX composition as a sub-clinical amount, i.e. less than the amount generally  
XX found to be clinically effective when the agent is administered alone.  
XX The composition is used in claimed methods of: inhibiting cell rolling,  
XX inflammation, thrombosis, restenosis, metastasis, the growth and/or  
XX replication of tumor cells or leukemia cells, an increase in number of  
XX tumor or leukemia cells, cell-cell, cell-matrix, platelet-matrix,  
XX platelet-platelet and/or cell-platelet complex formation, aggregation or  
XX adhesion, increasing the mortality rate of tumor or leukemia cells, the  
XX susceptibility of disease cells to damage by anti-disease agents, and the  
XX susceptibility of tumor or leukemia cells to damage by anti-cancer  
XX agents; and ameliorating the effects of a disease, preventing a disease,  
XX treating a disease or inhibiting the progress of a disease.  
XX  
XX Sequence 277 AA;  
SQ  
Query Match 100.0%; Score 576; DB 8; Length 277;  
Best Local Similarity 100.0%; Pred. No. 6.9e-35;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SEITDPAVSVALGQTVRTICGDSLSRSYYASWYQKPGAPVLYIGKNNRPSGIDRF 60  
DB 153 SEITDPAVSVALGQTVRTICGDSLSRSYYASWYQKPGAPVLYIGKNNRPSGIDRF 212  
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFVGGGTCLTVLGA 111  
DB 213 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFVGGGTCLTVLGA 263  
RESULT 14  
AD128367  
ID AD128367 standard; protein; 278 AA.  
XX  
XX AD128367;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Human scfv fragment Y17, binds to platelets.  
DE

XX Human; antibody; scfv; platelet; drug delivery; cancer; therapy.  
XX  
XX Homo sapiens.  
OS  
XX MO2004002528-A1.  
XX  
XX 08-JAN-2004.  
XX  
XX 30-JUN-2003; 2003MO-US020604.  
XX  
XX 01-JUL-2002; 2002US-00189025.  
XX  
XX (SAVI-) SAVIENT PHARM INC.  
XX  
XX Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;  
XX WPI; 2004-099189/10.  
XX  
XX Composition comprising an agent and/or antibody or its fragment, useful  
XX for treating auto-immune disease, thrombosis, restenosis, metastasis, or  
XX PT for inhibiting growth and/or replication of tumor cells or leukemia  
XX cells.  
XX  
XX Claim 13; SEQ ID NO 2; 58pp; English.  
XX  
XX The present sequence is the protein sequence of human scfv fragment Y17.  
XX This antibody was identified by screening a human antibody phage library  
XX that has diversity only in the heavy chain CDR3 regions. Fixed human  
XX platelets were screened in order to identify antibodies that bind  
XX platelets. Y17 binds leukemic cells. The invention relates to  
XX compositions utilising an agent and an antibody or its fragment. The  
XX agent is a toxin, radioisotope or pharmaceutical agent such as  
XX doxorubicin. It is complexed or combined with or conjugated to the  
XX antibody or its fragment. The agent and/or antibody can be present in the  
XX composition as a sub-clinical amount, i.e. less than the amount generally  
XX found to be clinically effective when the agent is administered alone.  
XX The composition is used in claimed methods of: inhibiting cell rolling,  
XX inflammation, thrombosis, restenosis, metastasis, the growth and/or  
XX replication of tumor cells or leukemia cells, an increase in number of  
XX tumor or leukemia cells, cell-cell, cell-matrix, platelet-matrix,  
XX platelet-platelet and/or cell-platelet complex formation, aggregation or  
XX adhesion, increasing the mortality rate of tumor or leukemia cells, the  
XX susceptibility of disease cells to damage by anti-disease agents, and the  
XX susceptibility of tumor or leukemia cells to damage by anti-cancer  
XX agents; and ameliorating the effects of a disease, preventing a disease,  
XX treating a disease or inhibiting the progress of a disease.  
XX  
XX Sequence 278 AA;  
SQ  
Query Match 100.0%; Score 576; DB 8; Length 278;  
Best Local Similarity 100.0%; Pred. No. 6.9e-35;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SEITDPAVSVALGQTVRTICGDSLSRSYYASWYQKPGAPVLYIGKNNRPSGIDRF 60  
DB 154 SEITDPAVSVALGQTVRTICGDSLSRSYYASWYQKPGAPVLYIGKNNRPSGIDRF 213  
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFVGGGTCLTVLGA 111  
DB 214 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFVGGGTCLTVLGA 264  
RESULT 15  
AAE02186  
ID AAE02186 standard; protein; 280 AA.  
XX  
XX AAE02186;  
XX  
XX 10-AUG-2001 (first entry)  
XX  
XX PAM2 single chain variable region (scfv) antibody.  
DE

Job time : 71.0521 secs

KM Pectin; PAM1 antibody; single chain variable region; scFv; food; jam;  
 KM yogurt; gel; homogalacturonan; HG; plant cell wall.  
 XX  
 OS Unidentified.

Key	Location/Qualifiers
FT Peptide	1..22
FT	/label= pelB_leader_sequence
FT Region	23..138
FT	/label= Heavy_chain_fragment
FT Region	139..154
FT	/label= Linker
FT	155..275
FT Region	/label= Light_chain_fragment
FT	265..275
FT	/label= Myc_epitope
FT Misc-difference	279..80
FT	/note= "Encoded by TAGACT"

US6228599-B1.

08-MAY-2001.

26-FEB-1999; 99US-00260527.

24-DEC-1998; 98GB-00028700.

(DANIT-) DANISCO AS.

Knox JP, Willats WGT, Mikkelsen JD;

WPI; 2001-342672/36.

N-PSDB; AAD06194.

PT New PAM1 and PAM2 antibodies capable of binding de-esterified  
 PT homogalacturonan, useful for identifying a pectin moiety, for quantifying  
 PT the amount of pectin in a sample or for extracting pectin from a sample.

PS Claim 2; Fig 4B; 21pp; English.

CC The invention relates to antibodies specific to pectin, such as PAM1 and  
 CC PAM2 scFv (single chain variable region). These antibodies are derived  
 CC from a naive phage display library known as the synthetic scFv library  
 CC (#1). PAM1 and PAM2 antibodies are capable of binding to de-esterified  
 CC and un-substituted homogalacturonan (HG), useful for identifying a pectin  
 CC motif. PAM antibody is useful for identifying a pectin functional group  
 CC and in assays to determine if a particular pectin composition has the  
 CC pectin motif or can be used to prepare a food for human and animal  
 CC consumption, such as jams, yogurts or gels. The PAM antibodies are  
 CC further useful for quantifying the amount of pectin in a sample or for  
 CC extracting pectin from a sample. PAM antibodies are also used to identify  
 CC de-esterified homogalacturonan blocks in the primary cell walls of  
 CC plants. The present sequence is PAM2 scFv antibody specific to pectin.  
 CC Note: This sequence is stated as being the same as that shown as SEQ ID  
 CC NO: 3 in the sequence listing of the specification, however the sequence  
 CC has 2 extra residues at the C-terminal end

SQ Sequence 280 AA;

Query Match 100.0%; Score 576; DB 4; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 7e-35;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTDDPAVSAIGQTVIRITCGDLSRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60  
 DB 154 SELTDDPAVSAIGQTVIRITCGDLSRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 213

QY 61 SSSSGNTASTLTGAQAEADADYCNRSRDSGNHVVFGGTKLTVLGAA 111  
 DB 214 SSSSGNTASTLTGAQAEADADYCNRSRDSGNHVVFGGTKLTVLGAA 264

Search completed: April 25, 2005, 20:22:17

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```
/ Sequence 7, Application US/10029988B
/ Publication No. US20040001839A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPTIOPES CONTAINING SULFATED
/ MOIETIES, ANTIBODIES TO SUCH EPTIOPES, AND USES THEREOF
/ FILE REFERENCE: 10793/46
/ CURRENT APPLICATION NUMBER: US/10/029,988B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 7
/ LENGTH: 111
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-029-988B-7
```

```
Query Match          100.0%; Score 576; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SELTOPPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 1 SELTOPPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
```

```
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
```

## RESULT 3

```
US-10-032-423A-7
/ Sequence 7, Application US/10032423A
/ Publication No. US20040002450A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPTIOPES CONTAINING SULFATED
/ MOIETIES, ANTIBODIES TO SUCH EPTIOPES, AND USES THEREOF
/ FILE REFERENCE: 10793/45
/ CURRENT APPLICATION NUMBER: US/10/032,423A
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 12/29/2000
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 7
/ LENGTH: 111
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-032-423A-7
```

```
Query Match          100.0%; Score 576; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SELTOPPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 1 SELTOPPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
```

```
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
```

## RESULT 4

```
US-10-029-926B-7
/ Sequence 7, Application US/10029926B
/ Publication No. US20040073011A1
/ GENERAL INFORMATION:
/ APPLICANT: HAANY, et al.
/ TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
```

```
/ FILE REFERENCE: 10793/50
/ CURRENT APPLICATION NUMBER: US/10/029,926B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 12/29/2000
/ NUMBER OF SEQ ID NOS: 203
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 7
/ LENGTH: 111
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-029-926B-7
```

```
Query Match          100.0%; Score 576; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.1e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SELTOPPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 1 SELTOPPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
```

```
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
```

## RESULT 5

```
US-10-888-959-8
/ Sequence 8, Application US/10888959
/ Publication No. US20050048545A1
/ GENERAL INFORMATION:
/ APPLICANT: Cull, Millard
/ APPLICANT: Brennan, Miles
/ APPLICANT: Gill, Ronald
/ TITLE OF INVENTION: Universal Detection of Binding
/ FILE REFERENCE: BPP 03
/ CURRENT APPLICATION NUMBER: US/10/888,959
/ CURRENT FILING DATE: 2004-07-09
/ PRIOR APPLICATION NUMBER: US 60/487,018
/ PRIOR FILING DATE: 2003-07-10
/ PRIOR APPLICATION NUMBER: US 60/509,196
/ PRIOR FILING DATE: 2003-10-06
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 8
/ LENGTH: 125
/ TYPE: PRT
/ ORGANISM: Artificial
/ OTHER INFORMATION: variable light chain domain
US-10-888-959-8
```

```
Query Match          100.0%; Score 576; DB 17; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.5e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SELTOPPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 1 SELTOPPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
```

```
QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
DB 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLGAAA 111
```

## RESULT 6

```
US-10-032-037B-204
/ Sequence 204, Application US/10032037B
/ Publication No. US20040001822A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPTIOPES CONTAINING SULFATED
/ MOIETIES, ANTIBODIES TO SUCH EPTIOPES, AND USES THEREOF
```



```
/ FILE REFERENCE: 10793/44
/ CURRENT APPLICATION NUMBER: US/10/032.037B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 204
/ LENGTH: 266
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-032-037B-204

Query Match          100.0%; Score 576; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 7.7e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTODPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 153 SELTODPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212
213 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGCTKLTVLGAAA 111

RESULT 7
US-10-029-988B-204
/ Sequence 204, Application US/10029988B
/ Publication No. US20040001839A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPTIOPES CONTAINING SULFATED
/ FILE REFERENCE: 10793/46
/ CURRENT APPLICATION NUMBER: US/10/029.988B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 204
/ LENGTH: 266
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-029-988B-204

Query Match          100.0%; Score 576; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 7.7e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTODPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 153 SELTODPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212
213 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGCTKLTVLGAAA 111

RESULT 8
US-10-032-423A-204
/ Sequence 204, Application US/10032423A
/ Publication No. US20040002450A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPTIOPES CONTAINING SULFATED
/ FILE REFERENCE: 10793/45
/ CURRENT APPLICATION NUMBER: US/10/032.423A
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 12/29/2000
```

```
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 204
/ LENGTH: 266
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-032-423A-204

Query Match          100.0%; Score 576; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 7.7e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTODPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 153 SELTODPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212
213 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGCTKLTVLGAAA 111

RESULT 9
US-10-032-037B-25
/ Sequence 25, Application US/10032037B
/ Publication No. US20040001822A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPTIOPES CONTAINING SULFATED
/ FILE REFERENCE: 10793/44
/ CURRENT APPLICATION NUMBER: US/10/032.037B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 25
/ LENGTH: 277
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-032-037B-25

Query Match          100.0%; Score 576; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 8e-44;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTODPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 153 SELTODPAVSVALGQTVRITCGDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212
213 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGCTKLTVLGAAA 263

RESULT 10
US-10-032-037B-203
/ Sequence 203, Application US/10032037B
/ Publication No. US20040001822A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPTIOPES CONTAINING SULFATED
/ FILE REFERENCE: 10793/44
/ CURRENT APPLICATION NUMBER: US/10/032.037B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 203
/ LENGTH: 277
/ TYPE: PRF
```

```
; ORGANISM: Homo sapiens
US-10-032-037B-203

Query Match
Best Local Similarity 100.0%; Score 576; DB 15; Length 277;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTDPAAVVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 153 SELTDPAAVVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212

QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLGAAA 111
DB 213 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLGAAA 263

RESULT 11
US-10-029-988B-25
; Sequence 25, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-029-988B-25

Query Match
Best Local Similarity 100.0%; Score 576; DB 15; Length 277;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTDPAAVVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 153 SELTDPAAVVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212

QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLGAAA 111
DB 213 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLGAAA 263

RESULT 12
US-10-029-988B-203
; Sequence 203, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-029-988B-203

Query Match
Best Local Similarity 100.0%; Score 576; DB 15; Length 277;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTDPAAVVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 153 SELTDPAAVVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212

QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLGAAA 111
DB 213 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLGAAA 263

RESULT 13
US-10-032-423A-25
; Sequence 25, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-032-423A-25

Query Match
Best Local Similarity 100.0%; Score 576; DB 15; Length 277;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTDPAAVVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 153 SELTDPAAVVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212

QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLGAAA 111
DB 213 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFPGGKTLTVLGAAA 263

RESULT 14
US-10-032-423A-203
; Sequence 203, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-032-423A-203

Query Match
Best Local Similarity 100.0%; Score 576; DB 15; Length 277;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SELTDPAAVVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60
DB 153 SELTDPAAVVALGQTVRITTCQDLSRSYYASWYQKPGQAPVLVIYGNRRPSGIPDRF 212
```

Qy 61 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVLGAA 111  
 |||||  
 Db 213 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVLGAA 263

RESULT 15  
 US-10-029-926B-25  
 ; Sequence 25, Application US/10029926B  
 ; Publication No. US20040073011A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HAGAY, et al.  
 ; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY  
 ; FILE REFERENCE: 10793/50  
 ; CURRENT APPLICATION NUMBER: US/10/029,926B  
 ; PRIOR FILING DATE: 2001-12-31  
 ; PRIOR APPLICATION NUMBER: 60/258,948  
 ; NUMBER OF SEQ ID NOS: 203  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 25  
 ; LENGTH: 277  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-029-926B-25

Query Match 100.0%; Score 576; DB 15; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 8e-44;  
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SELTOPPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLYTYGKNNRPSGIPDRF 60  
 |||||  
 Db 153 SELTOPPAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLYTYGKNNRPSGIPDRF 212  
 |||||  
 Qy 61 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVLGAA 111  
 |||||  
 Db 213 SSSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVLGAA 263

Search completed: April 25, 2005, 21:09:46  
 Job time : 50.1009 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: April 25, 2005, 19:57:16 ; Search time 12.7982 Seconds  
(Without alignments)  
834.495 Million cell updates/sec

Title: US-10-029-926d-7

Perfect score: 576

Sequence: 1 SEITOPPAVSVALGQTVRT.....SGNHVFGGKTLTVGAAA 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	564	97.9	109	2	SI9663
2	558	96.9	108	2	S47184
3	547.5	95.1	110	2	S36272
4	542	94.1	127	2	S70444
5	541	93.9	108	2	S38498
6	535	92.9	109	2	S38496
7	537	91.5	108	1	L3HUSH
8	526	91.3	233	2	S25748
9	517.5	89.8	146	2	S02083
10	514.5	89.3	110	2	S19672
11	499	86.6	96	2	S36060
12	489	86.6	115	2	S13726
13	488	86.5	233	2	S25741
14	438.5	76.1	106	2	S38493
15	420	72.9	105	2	S49533
16	414	71.2	190	2	S25740
17	410	71.2	119	2	S30526
18	397	68.9	107	2	PC4283
19	395.5	68.7	120	2	S30525
20	384	66.7	226	2	S25745
21	381	66.1	231	2	S25751
22	376	65.3	120	2	S25738
23	376	65.3	120	2	S30527
24	376	65.3	151	2	S25739
25	376	65.3	231	2	S25753
26	374	64.9	233	2	S25747
27	373.5	64.8	212	2	S70431
28	370	64.2	107	1	L4H0HL
29	370	64.2	108	1	L5H0DL

30	369	64.1	106	1	L4H0BU	Ig lambda chain V-
31	367	63.7	132	2	S09713	Ig lambda chain V
32	365.5	63.5	112	2	S51148	antibody light cha
33	363.5	63.1	232	2	S25756	Ig lambda chain -
34	362	62.8	106	1	L4H0ML	Ig lambda chain V-
35	358	62.2	106	1	L4H0X	Ig lambda chain V-
36	355	61.6	109	2	S68171	Ig lambda chain V
37	353	61.3	111	2	S36274	Ig lambda chain V
38	353	61.3	128	2	S24319	Ig lambda chain pr
39	346	60.1	105	2	S44124	Ig lambda chain V
40	344	59.7	235	2	S05270	Ig lambda chain pr
41	343	59.5	111	2	S47009	Ig lambda chain V1
42	342	59.4	111	1	L2H0MC	Ig lambda chain V-
43	341	59.2	95	2	S36065	Ig lambda chain -
44	341	59.2	114	2	S16440	Ig lambda chain V-
45	340	59.0	106	1	L4H0XN	Ig lambda chain V-

## ALIGNMENTS

## RESULT 1

SI9663  
Ig lambda chain V region (clone alpha-BSA3) - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
C/Accession: SI9663  
R/Mark: J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter  
J. Mol. Biol. 222, 581-597, 1991  
A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p  
A/Reference number: SI9663; PMID:92085276; PMID:1748994  
A/Accession: SI9663  
A/Molecule type: mRNA  
A/Residues: 1109 <MRA>  
A/Cross-references: EMBL:X61640; NID:G29492; PIDN:CAA3821.1; PID:q1340166  
C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/15-89/Domain: immunoglobulin homology <IMM>

## Query Match

Best Local Similarity 97.9%; Score 564; DB 2; Length 109;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITOPPAVSVALGQTVRTICGDSLSRYASVYQKPGQAPVLYTKNNRPSGIPDRF 60  
DB 2 SEITOPPAVSVALGQTVRTICGDSLSRYASVYQKPGQAPVLYTKNNRPSGIPDRF 61

QY 61 SGGSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFSGGKTLTVLG 108  
DB 62 SGGSSGNTASLTITGAQAEDEADYCNRSRDSGNHVFSGGKTLTVLG 109

## RESULT 2

S47184  
Ig lambda chain - human

C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C/Accession: S47184  
R/Mark: R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.

A/Title: Submitted to the EMBL Data Library, June 1994  
A/Description: Cloning and analysis of Igm anti-thyroglobulin autoantibodies from patient

A/Reference number: S47181  
A/Accession: S47184

A/Status: Preliminary  
A/Molecule type: mRNA

A/Residues: 1-108 <MCI>  
A/Cross-references: EMBL:X79783; NID:G506426; PIDN:CAA56179.1; PID:G506427

C/Keywords: heterotetramer; immunoglobulin  
F/15-89/Domain: immunoglobulin homology <IMM>

## Query Match

Best Local Similarity 96.9%; Score 558; DB 2; Length 108;  
Matches 100.0%; Pred. No. 5.8e-41;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQVTRITCGDSLRSYYASWYQKPGQAPVLYVYGNKRRPSGIPDRF 60

Db 2 SEITDPAVSVALGQVTRITCGDSLRSYYASWYQKPGQAPVLYVYGNKRRPSGIPDRF 61

QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVL 107

Db 62 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVL 108

### RESULT 3

S36272

Ig lambda chain V region (clone alpha-THY-29) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000

C/Accession: S36272

R/Griffiths, A.D.; Malngvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A/Title: Human anti-self antibodies with high specificity from phage display libraries.

A/Reference number: S36256; MID:9318448; PMID:7679990

A/Accession: S36272

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-110 <GRI>

A/Status: preliminary; nucleic acid sequence not shown

A/Status: preliminary; nucleic acid sequence not shown

A/Status: preliminary; nucleic acid sequence not shown

A/Status: preliminary; nucleic acid sequence not shown

A/Status: preliminary; nucleic acid sequence not shown

A/Status: preliminary; nucleic acid sequence not shown

A/Status: preliminary; nucleic acid sequence not shown

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A/Status: preliminary; nucleic acid sequence not shown

A/Status: preliminary; nucleic acid sequence not shown

A/Status: preliminary; nucleic acid sequence not shown

A/Status: preliminary; nucleic acid sequence not shown

A/Status: preliminary; nucleic acid sequence not shown

Query Match 94.1%; Score 542; DB 2; Length 127;

Best Local Similarity 97.2%; Pred. No. 1.6e-39;

Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQVTRITCGDSLRSYYASWYQKPGQAPVLYVYGNKRRPSGIPDRF 60

Db 21 SEITDPAVSVALGQVTRITCGDSLRSYYASWYQKPGQAPVLYVYGNKRRPSGIPDRF 80

QY 61 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVL 107

Db 81 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVL 127

### RESULT 5

S38498

Ig lambda chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C/Accession: S38498

R/Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorlick, B.D.; Voak, D.; Thorpe, J.

submitted to the EMBL Data Library, June 1993

A/Description: Human antibody fragments specific for human blood group antigens from a

A/Reference number: S38488

A/Accession: S38498

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-108 <MAR>

A/Status: preliminary

A/Status: preliminary

A/Status: preliminary

A/Status: preliminary

A/Status: preliminary

A/Status: preliminary

A/Status: preliminary

A/Status: preliminary

A/Status: preliminary

A/Status: preliminary

A/Status: preliminary

A/Status: preliminary

A/Status: preliminary

A/Status: preliminary

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A/Status: preliminary

A/Status: preliminary

A/Status: preliminary

A/Status: preliminary



A/Accession: S36060  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-96 <ML>  
A/Cross-references: EMBL:Z22202; NID:g312325; PIDN:CAA80211.1; PID:g312326  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 499; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 5.6e-36;  
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQTVRITTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 60  
DB 2 SEITDPAVSVALGQTVRITTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 61

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNH 95  
DB 62 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNH 96

RESULT 12  
S13726

Ig lambda chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S13726  
R:Ripplac, J.P.; Chuchana, P.; Bernard, F.; Bulwela, L.; Lefranc, G.; Lefranc, M.P.  
Nucleic Acids Res. 18, 7134, 1990  
A/Title: First genomic sequence of a human Ig variable lambda gene belonging to subgroup  
A/Reference number: S13726; MUID:91088295; PMID:2124677  
A/Accession: S13726  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-115 <PRI>  
A/Cross-references: EMBL:X56178; NID:g33404; PIDN:CAA39639.1; PID:g33405  
C/Genetics:  
A/Intons: 16/1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 499; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 6.7e-36;  
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQTVRITTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 60  
DB 21 SEITDPAVSVALGQTVRITTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 80

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNH 95  
DB 81 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNH 115

RESULT 13  
S25741

Ig lambda chain - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C/Accession: S25741  
R:Combrlato, G.; Klobbeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam  
A/Reference number: S16439; MUID:91257162; PMID:1904362  
A/Accession: S25741  
A/Status: preliminary; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-233 <COM>  
A/Cross-references: EMBL:X57805; NID:g33707; PIDN:CAA40943.1; PID:g33708  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 498; DB 2; Length 233;  
Best Local Similarity 86.9%; Pred. No. 1.6e-35;  
Matches 93; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 SEITDPAVSVALGQTVRITTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 60  
DB 21 SEITDPAVSVALGQTVRITTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 80

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFEGGTRITVL 107  
DB 81 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFEGGTRITVL 127

RESULT 14  
S38495

Ig lambda chain - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C/Accession: S38495  
R:Marke, J.D.; Ouwehand, W.H.; Bye, J.M.; Finern, R.; Gorick, B.D.; Voak, D.; Thorpe, J.  
Submitted to the EMBL Data Library, June 1993  
A/Description: Human antibody fragments specific for human blood group antigens from a  
A/Reference number: S38488  
A/Accession: S38495  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-106 <MAR>  
A/Cross-references: EMBL:Z23029; NID:g414037; PIDN:CAA80564.1; PID:g414038  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 438.5; DB 2; Length 106;  
Best Local Similarity 78.7%; Pred. No. 8.9e-31;  
Matches 85; Conservative 11; Mismatches 9; Indels 3; Gaps 1;

QY 1 SEITDPAVSVALGQTVRITTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 60  
DB 2 SEITDPAVSVALGQTVRITTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRF 61

QY 61 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFEGGTRITVL 108  
DB 62 SSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFEGGTRITVL 106

RESULT 15  
S49533

anti-5m antibody VL chain (V lambda 3b/J lambda 2/3) - human  
C/Species: Homo sapiens (man)  
C/Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 21-Jan-2000  
C/Accession: S49533  
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.  
Submitted to the EMBL Data Library, October 1994  
A/Description: Molecular characterization of natural human anti-5m autoantibodies.  
A/Reference number: S48797  
A/Accession: S49533  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-105 <MAH>  
A/Cross-references: EMBL:Z46346; NID:g560845; PIDN:CAA86465.1; PID:g1340169  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
F:11-85/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 420; DB 2; Length 105;  
Best Local Similarity 76.2%; Pred. No. 3.4e-29;  
Matches 80; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 4 TDDPAVSVALGQTVRITTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRPSGS 63  
DB 1 TDDPAVSVALGQTVRITTCGDSLSRSYYASWYQKPGQAPVLYYGKNNRPSGIPDRPSGS 60



Tue Apr 26 17:12:05 2005

us-10-029-926d-7.rpr

Page 5

Qy 64 SSGNTASLTTTGAQAEDEADYCNRSRDSGNHVFPGGTXLTVLG 108  
Db 61 SSGTIVTLTIFISGVQAEDEADYCOASDSSGTYVVFPGGTXLTVLG 105

Search completed: April 25, 2005, 20:24:06  
Job time : 13.7982 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:10:00 ; Search time 57.3459 Seconds

(without alignments)  
991.192 Million cell updates/sec

Title: US-10-029-926d-7

Perfect score: 576

Sequence: 1 SEITQDPAVSVALGQTVRIT.....SGNHVFGGQTKLVLGAAA 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	552	95.8	107	2 Q9NSD6	Q9NSD6 homo sapien
2	527	91.5	108	1 LV3A_HUMAN	P01714 homo sapien
3	526	91.3	233	2 Q6GMW4	Q6GMW4 homo sapien
4	427	74.1	233	2 Q8TBC9	Q8TBC9 homo sapien
5	422	73.3	81	2 Q7Z2E8	Q7Z2E8 homo sapien
6	416	72.2	233	2 Q8NSF4	Q8NSF4 homo sapien
7	379.5	65.9	234	2 Q8N355	Q8N355 homo sapien
8	377	65.5	111	1 LV3B_HUMAN	P80748 homo sapien
9	370	64.2	107	1 LV4C_HUMAN	P01717 homo sapien
10	370	64.2	108	1 LV5A_HUMAN	P01719 homo sapien
11	369.5	64.1	107	2 Q9UL82	Q9UL82 homo sapien
12	369	64.1	106	1 LV4A_HUMAN	P01715 homo sapien
13	362	62.8	106	1 LV4E_HUMAN	P06889 homo sapien
14	360.5	62.6	236	2 Q6GMW4	Q6GMW4 homo sapien
15	360	62.5	233	2 Q6NS96	Q6NS96 homo sapien
16	358	62.2	106	1 LV4B_HUMAN	P01716 homo sapien
17	355.5	61.7	236	2 Q6IPQ0	Q6IPQ0 homo sapien
18	348.5	60.5	234	2 Q6NS95	Q6NS95 homo sapien
19	347.5	60.3	233	2 Q6PUJ3	Q6PUJ3 homo sapien
20	344	59.7	235	2 Q6PIK1	Q6PIK1 homo sapien
21	342	59.4	111	1 LV2F_HUMAN	P01709 homo sapien
22	341.5	59.3	234	2 Q6GMW3	Q6GMW3 homo sapien
23	341.5	59.3	236	2 Q96E61	Q96E61 homo sapien
24	340	59.0	106	1 LV4D_HUMAN	P01718 homo sapien
25	339.5	58.9	234	2 Q6GMW8	Q6GMW8 homo sapien
26	337	58.5	111	1 LV2H_HUMAN	P01711 homo sapien
27	335.5	58.2	236	2 Q6PI07	Q6PI07 homo sapien
28	335	58.2	116	2 Q96UD0	Q96UD0 homo sapien
29	335	58.2	130	1 LV1G_HUMAN	P06310 homo sapien
30	331.5	57.6	112	1 LV2K_HUMAN	P04209 homo sapien
31	331	57.5	235	2 Q6IN99	Q6IN99 homo sapien

32	329	57.1	111	1 LV1D_HUMAN	P01702 homo sapien
33	328	56.9	111	1 LV7A_HUMAN	P01720 homo sapien
34	327.5	56.9	234	2 Q7Z2U7	Q7Z2U7 homo sapien
35	326	56.6	231	2 Q6GNB8	Q6GNB8 xenopus lae
36	325.5	56.5	112	2 Q96UD1	Q96UD1 homo sapien
37	325	56.4	111	1 LV2G_HUMAN	P01710 homo sapien
38	323	56.1	110	2 Q8TE63	Q8TE63 homo sapien
39	322.5	56.0	236	2 Q6GMX3	Q6GMX3 homo sapien
40	322	55.9	111	1 LV1C_HUMAN	P01701 homo sapien
41	321.5	55.8	112	1 LV6A_HUMAN	P01721 homo sapien
42	321.5	55.8	236	2 Q6PS53	Q6PS53 homo sapien
43	320.5	55.6	236	2 Q8NEJ1	Q8NEJ1 homo sapien
44	320	55.6	111	1 LV2C_HUMAN	P01706 homo sapien
45	319	55.4	233	2 Q6GNH3	Q6GNH3 xenopus lae

## ALIGNMENTS

### RESULT 1

ID	Q9NSD6	PRELIMINARY;	PRT;	107 AA.
AC	Q9NSD6;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Homo sapiens This CDS feature is included to show the translation of the corresponding V_region. Presently translation qualifiers on DE V_region features are illegal. (fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymphocyte;			
RA	Hohmann A.;			
RL	Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; L43092; AAA69746.2; ..			
DR	PIR; S70444; S70444.			
DR	HSSP; P01709; 2MCG.			
DR	InterPro; IPR007110; IG_1like.			
DR	InterPro; IPR003596; IG_V.			
DR	SMART; SM00406; IGV; 1.			
FT	PROSITE; PS50835; IG_LIKE; 1.			
FT	NON_TER 1			
FT	NON_TER 107			
FT	SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;			
QY	Query Match	95.8%;	Score 552;	DB 2; Length 107;
QY	Best Local Similarity	98.1%;	Pred. No. 5.4e-47;	
QY	Matches 105; Conservative	0;	Mismatches 2;	Indels 0; Gaps 0;
Db	1 ELTQDPAVSVALGQTVRITQSGDLSLSYSAWQQRKGQAPLVITGKNNRPSGIPDRFS 61			
QY	62 GSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVVFGGQTKLVLG 108			
Db	61 GSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVVFGGQTKLVLG 107			
RESULT 2				
LV3A_HUMAN	STANDARD;	PRT;	108 AA.	
ID	LV3A_HUMAN			
AC	P01714;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	05-JUL-1986 (Rel. 01, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	IG lambda chain V-III region SH.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70166723; PubMed=4909564;
RT Titani K., Wikier M., Shinoda T., Putnam F.W.;
RA "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT complete amino acid sequence and the location of the disulfide
bridges."
RL J. Biol. Chem. 245:2171-2176(1970).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01980; L3HUSH.
DR HSSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00447; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KM Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 97 Ig-like.
FT DISULFID 21 86
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;

Query Match 91.5%; Score 527; DB 1; Length 108;
Best Local Similarity 92.6%; Pred. No. 1,6e-44;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 SETTOPPAVSVALGQVVRITCGDSLRSYYASWYQOKPQAPLVLYGKNNRPSGIPDRF 60
DB 1 SETTOPPAVSVALGQVVRITCGDSLRSYYASWYQOKPQAPLVLYGKNNRPSGIPDRF 60
QY 61 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNNHVFPGGTLTYLG 108
DB 61 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNNHVFPGGTLTYLG 108

RESULT 3
Q6GMW4 PRELIMINARY; PRT; 233 AA.
AC 06GMW4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypoetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalski U., Smallus D.E., Scherch A., Schein J.B.,

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RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073786; AAH73786.1; -.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:006118; P:electron transport; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR006662; Thiolred.
DR Pfam; PF07654; C1-sec; 1.
DR Pfam; PF00447; Ig; 2.
DR PRINTS; PR00421; THIOREDOXIN.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KM Hypoetical protein.
SQ SEQUENCE 233 AA; 24855 MW; 462677B3B8FDE5BD CRC64;

Query Match 91.3%; Score 526; DB 2; Length 233;
Best Local Similarity 91.7%; Pred. No. 4,8e-44;
Matches 99; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 SETTOPPAVSVALGQVVRITCGDSLRSYYASWYQOKPQAPLVLYGKNNRPSGIPDRF 60
DB 21 SETTOPPAVSVALGQVVRITCGDSLRSYYASWYQOKPQAPLVLYGKNNRPSGIPDRF 80
QY 61 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNNHVFPGGTLTYLG 108
DB 81 SGSSSGNTASLTITGAQAEDEADYCNRSRDSGNNHVFPGGTLTYLG 128

RESULT 4
Q8TBC9 PRELIMINARY; PRT; 233 AA.
AC 08TBC9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypoetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C.,

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RA Krzywnski M.I., Skalka U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Straubeberg R.;
RU Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022823; AAH22823.1; -
DR PIR; S12442; S12442.
DR PIR; S30525; S30525.
DR PIR; S30526; S30526.
DR HSSP; P01842; 1LIL.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-sect; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR Hypothetical protein.
SQ SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;

Query Match 74.1%; Score 427; DB 2; Length 233;
Best Local Similarity 76.8%; Pred. No. 3.2e-33;
Matches 82; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 2 ELTQDPAVSVALGQTVRITCGDLSRSYASWTQKPGAPVLVIYKNNRPSGIDPRFS 61
DB 22 ELTQPSVSVPQGTARITCSGDALPKQYKVMYQKKGAPVLVIYKNNRPSGIDPRFS 81
QY 62 GSSSGTASITITGAQDEADYVYCNRSDDSGNNHVFVGSGTKTLTVLG 108
DB 82 GSSSGTAVTITIGVQDEADYVYCNRSDDSGNNHVFVGSGTKTLTVLG 128

RESULT 5
QY 0722E8 PRELIMINARY; PRT; 81 AA.
AC 0722E8;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Rearranged VJ13 segment (Rearranged VJ13 gene segment)
DE (Fragment).
GN Name=VJ13;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBT_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hodgkin Lymphoma, and Mantle cell Lymphoma;
RA Tingiely M., Rosenquist R., Sundstrom C., Amant R.M., Koppers R.,
RA Handmann M.U., Brauninger A.;
RU Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564423; CAD92030.1; -
DR EMBL; AJ564424; CAD92031.1; -
DR HSSP; P01709; 1DCL.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 81 AA; 8702 MW; CFF1D466B794C9F CRC64;

Query Match 73.3%; Score 422; DB 2; Length 81;
Best Local Similarity 96.3%; Pred. No. 3.1e-34;
Matches 78; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 19 ITTCGDSLSRSYASWTQKPGAPVLVIYKNNRPSGIDPRFGSSSGTASITITGAQA 78
DB 1 ITTCGDSLSRSYASWTQKPGAPVLVIYKNNRPSGIDPRFGSSSGTASITITGAQA 60
QY 79 EDEADYVYCNRSDDSGNNHVFVG 99
DB 61 EDEADYVYCNRSDDSGNNHVFVG 81

RESULT 6
QY 08NSP4 PRELIMINARY; PRT; 233 AA.
AC 08NSP4;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBT_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow R.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnski M.I., Skalka U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Straubeberg R.;
RU Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032452; AAH32452.1; -
DR PIR; A39949; A39949.
DR PIR; S12441; S12441.
DR PIR; S12443; S12443.
DR HSSP; P01842; 1LIL.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-sect; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR Hypothetical protein.
SQ SEQUENCE 233 AA; 24961 MW; F092CFBAA6E3A9A CRC64;

Query Match 72.2%; Score 416; DB 2; Length 233;
Best Local Similarity 74.8%; Pred. No. 3.9e-33;
Matches 80; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

```

Db 22 ELTOPSVSVSGQTARITCGDAPLPRKAYWYQKSGQTPVLYVYDTERPSGIDPERPS 81  
QY 62 GSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFVGGGTCLTVLG 108  
Db 82 GSSSGTATLTITGSAQVEDEADYYCNSRDSGNHVFVGGGTCLTVLG 128

## RESULT 7

Q8N355 PRELIMINARY; PRT; 234 AA.  
ID 08N355;  
AC 08N355;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypochemical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McKernan P.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywicki M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC028090; AAH28090.1; -.  
DR PIR; S09713; S09713.  
DR PIR; S12441; S12441.  
DR PIR; S30527; S30527.  
DR HSSP; P01842; 1L1L.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig V.  
DR Pfam; PF07654; C1-set; 1.  
DR SMART; SM00406; IgV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 2.  
DR PROSITE; PSS0290; IG\_MHC; UNKNOWN\_1.  
KW Hypochemical protein.  
SQ SEQUENCE 234 AA; 24792 MW; CC848CABA4A9D63 CRC64;

Query Match 65.5%; Score 379.5; DB 2; Length 234;  
Best Local Similarity 70.1%; Pred. No. 1.3e-29;

Matches 75; Conservative 12; Mismatches 19; Indels 1; Gaps 1;

QY 3 LTODPAVVALGQVTRITCGDLSRSYASMYOQKPOQAVLYVYGNRPSGIDPRFSG 62  
Db 23 LTQPPSVSVAPGQTARITCGDNNIGSKSVYMQKPOQAVLYVYDSDPSPGIDPRFSG 82

QY 63 SSSGNTASLTITGAQAEDEADYYCNSRDSGNH-VVFGGTCLTVLG 108

Db 83 SNSGNTATLTITRVDADEADYYCOLMSSSDHPVVFVGGGTCLTVLG 129

## RESULT 8

LV3B HUMAN STANDARD; PRT; 111 AA.

ID LV3B\_HUMAN  
AC P80748;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 25-JAN-2005 (Rel. 46, Last annotation update)  
DE Ig lambda chain V-II region I01.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE, SUBUNIT, DISEASE, AND 3D-STRUCTURE MODELLING.  
RC TISSUE=Urine;  
RX MEDLINE=99441384; PubMed=10510403;  
RA Jokiranta T.S., Solomon A., Pangburn M.K., Zipfel P.F., Meri S.;  
RT "Nephriticogenic lambda light chain dimer: a unique human  
miniantibody against complement factor H";  
RL J. Immunol. 163:4590-4596(1999).  
CC -1- FUNCTION: Activates the alternative complement pathway by binding  
to the short consensus repeat domain 3 (SCR3) of factor H.  
CC -1- SUBUNIT: Homodimer.  
CC -1- DISEASE: The blocking of factor H by I01 protein leads to the  
developmental of membranoproliferative glomerulonephritis (MPGN).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PDB; 2DOI; Model; A/B=1-111.  
DR GO; GO:0005976; C:extracellular; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IgV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
DR 3D-structure; Direct protein sequencing; Immunoglobulin V region.  
KM DOMAIN 1 97  
FT SITE 48 51 SCR3 binding.  
FT BINDING 15 15 SCR3.  
FT BINDING 25 25 SCR3.  
FT BINDING 29 29 SCR3.  
FT BINDING 94 94 SCR3.  
FT DISULFID 21 86 By similarity.  
FT STRAND 4 4  
FT STRAND 8 8  
FT TURN 13 14  
FT STRAND 16 22  
FT STRAND 32 37  
FT TURN 38 40  
FT STRAND 41 46  
FT TURN 49 50  
FT STRAND 54 54  
FT TURN 55 55  
FT TURN 58 59  
FT STRAND 60 61  
FT STRAND 64 65  
FT TURN 66 67  
FT TURN 68 74  
FT TURN 78 79  
FT STRAND 82 88  
FT TURN 91 93  
FT STRAND 97 98  
FT STRAND 102 104  
FT TURN 107 108  
FT NON TER 111 111

SQ SEQUENCE 111 AA; 11935 MW; 69498BEBFDE82053 CRC64;

Query Match 65.5%; Score 377; DB 1; Length 111;  
Best Local Similarity 69.5%; Pred. No. 1.3e-29;



```

Query Match Similarity      64.1%; Score 369.5; DB 2; Length 107;
Best Local Similarity      69.8%; Pred. No. 6.7e-29;
Matches      74; Conservative      8; Mismatches      23; Indels      1; Gaps      1;

QY      2 ELTQDPAVSVALGQTVRTITCOGDSLRSYYASWYQKPGQAPLVLYTGKNNRPSGIPDRFS 61
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      3 ELTGSSVSVPSPGQARITITSGDILLAKKAYARFQKPGQAPILIVFKTERPSGIPDRFS 62
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      62 GSSSGNTASLTITGAQAEADYDYNCSKSDSGNHVFGGCTKLTVL 107
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      63 GSSSGTIVTLITSGAQVEADYCYSA-SDNNGRVPFGGCTKLTVL 107
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 12
LV4A_HUMAN          STANDARD;          PRT;          106 AA.
ID   LV4A_HUMAN          P01715;
DT   21-JUL-1986 (Rel. 01, Created)
DI   21-JUL-1986 (Rel. 01, Last sequence update)
DR   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig lambda chain V-IV region Bau.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RM   MEDLINE=75059189; PubMed=4435717;
RA   Baczko K., Braun D., Hilschmann N.;
RT   Pattern of antibody structure, the primary structure of monoclonal
RT   immunoglobulin L-chain of the lambda-type, subgroup IV (Bence-Jones
RT   protein Bau.).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 355:131-154(1974).
CC   -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01981; L4HUBU.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; IG-like.
DR   InterPro; IPR003596; IG_v.
DR   Pfam; PF00047; Ig_1.
DR   SMART; SM00406; Igv_1.
DR   PROSITE; PS50835; IG_LIKE_1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DOMAIN      1      102
FT   NON_TER     106
SQ   SEQUENCE      106 AA; 11305 MW; 4B6A688E0EC46571 CRC64;

Query Match
Best Local Similarity      64.1%; Score 369; DB 1; Length 106;
Matches      72; Conservative      11; Mismatches      21; Indels      2; Gaps      1

QY      3 LTQDPAVSVALGQTVRTITCOGDSLRSYYASWYQKPGQAPLVLYTGKNNRPSGIPDRSG 62
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      3 LTQPPSLVSPGQARITITSGDILLAKKAYARFQKPGQAPILIVFKTERPSGIPDRSG 62
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      63 SSSGNTASLTITGAQAEADYDYNCSKSDSGNHVFGGCTKLTVLG 108
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      63 SSSGTTIVTLITSGAQVEADYCYQKWDG--YTVIFGGGCTKLTVLG 106
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 13
LV4E_HUMAN          STANDARD;          PRT;          106 AA.
ID   LV4E_HUMAN          P06889;
DT   01-JAN-1988 (Rel. 06, Created)
DI   01-JAN-1988 (Rel. 06, Last sequence update)
DR   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig lambda chain V-IV region MOL.
OS   Homo sapiens (Human).

```

[illegible]



Query Match 66.6%; Score 360.5; DB 2; Length 236;  
 Best Local Similarity 66.7%; Pred. No. 1,3e-27;  
 Matches 74; Conservative 8; Mismatches 26; Indels 3; Gaps 1;

```

QY 1 SELPDPAVAVALGCTVATTCQGPLR---SYASVYQKQGAQAVVYVYKGNRRPSIP 57
DB 21 SVLPDPPEVSGAPGKRVATISCTGSSNIGAGDVHMYQQLPETAIRLITGNSNPPSGVP 80
QY 58 DRFGSSSGNTASLTITGAQADEADYVYCNRRDSSGNHVYFGGKTGLTVLG 108
DB 81 DRFGSGKGTASLTATITGLQADEADYVYCSVDSSLSGVMTGGGKTGLTVLG 131

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RA Krzywnski M.I., Skalka U., Smalhus D.E., Schnerch A., Schein J.E.,
RT Jones S.J., Marra M.A.; Initial analysis of more than 15,000 full-length human
RL "generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC
RA TISSUE=Lung;
RA Strauberg R.;
DR Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070352; AAH70352.1; -
DR HSSP; P01709; IABJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 24899 MW; D3B0A54F2972D473 CRC64;

Query Match 62.5%; Score 360; DB 2; Length 233;
Best Local Similarity 64.8%; Pred. No. 1.4e-27;
Matches 68; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

QY 3 LTDDPAVSVALGOTVRITTCGDSILRSYASWYQOKPQQAFLVLYIGKNRPSGIPDRFSG 62
DB 23 LTQPPSVSVAPGQTARITTCGNNIGSKSVHWYQOKPQQAFLVWVYDDSDRPSGIPERLSG 82
QY 63 SSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFEGGTRKLTVL 107
DB 83 SSSGNTATLTISRVEAGDEADYYCQWWDSTSNHVFEGTKVSVL 127

Search completed: April 25, 2005, 20:33:56
Job time : 59.3459 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 19:56:06 ; Search time 169.824 Seconds  
(without alignments)  
630.846 Million cell updates/sec

Title: US-10-029-926D-25

Perfect score: 1440

Sequence: 1 MKVLPPTAAAGLLLAQPA.....VLGAAAEQKLISEEDINGAA 277

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1980s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1440	100.0	277	5	ABG78150 Human Fv
2	1440	100.0	277	5	ABG91841 Human ant
3	1436	99.7	277	8	AD128366 Human scf
4	1416	98.3	277	5	ABG78328 Human Fv
5	1416	98.3	277	5	ABG92019 Human ant
6	1397.5	97.0	278	8	AD128367 Human scf
7	1393.5	96.8	280	8	ADJ57363 P-selecti
8	1386.5	96.3	280	8	AD128368 Human scf
9	1378	95.7	266	5	ABG92020 Human ant
10	1294	89.9	291	8	ADN06989 Human EFG
11	1278.5	88.8	282	4	AAE02185 PM1 sing
12	1275.5	88.6	309	2	AAW83322 Single ch
13	1275.5	88.6	309	5	ABB09603 Amino aci
14	1275.5	88.6	309	6	ABG74384 Single ch
15	1275.5	88.6	309	7	ADG98737 Human sin
16	1275.5	88.6	309	8	AD040446 Human sin
17	1257	87.3	246	5	ABG78329 Human Fv
18	1257	87.3	246	5	ABG92026 Antibody
19	1250	86.8	256	5	ABG78334 Human Fv
20	1250	86.8	256	5	ABG92025 Antibody
21	1231.5	85.5	260	5	ABG92023 Antibody
22	1223	84.6	263	5	ABG92024 Antibody
23	1218.5	84.6	239	7	ADG95753 Human Bly
24	1218.5	84.6	239	7	ADG95753 Single ch
25	1212.5	84.2	239	5	ABP46027 Human Bly

26	1212.5	84.2	239	7	ADG96854
27	1201.5	83.4	290	6	ABP55318
28	1201.5	83.4	290	7	AD199518
29	1194	82.9	312	2	AAW83323
30	1194	82.9	312	5	ABB09604
31	1194	82.9	312	6	ABG74385
32	1194	82.9	312	7	ADG98738
33	1194	82.9	312	8	AD040447
34	1191.5	82.7	239	5	ABP46004
35	1191.5	82.7	239	7	ADG96831
36	1191	82.7	291	5	AAE29202
37	1188.5	82.5	296	5	ABG60637
38	1188.5	82.5	296	7	AD199519
39	1186	82.4	291	5	ABG60632
40	1181	82.0	238	3	AAW95198
41	1178	81.8	244	6	AAO31136
42	1149	79.8	242	8	AD158068
43	1139.5	79.1	239	5	ABP46007
44	1139.5	79.1	239	7	ADG96834
45	1133	78.7	244	6	AAO31139

#### ALIGNMENTS

RESULT 1  
ABG78150  
ID ABG78150 standard; protein; 277 AA.

AC ABG78150;

DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #25.

XX Human Fv molecule; hypervariable region; single chain Fv; cytostatic;

KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukemia; adenoma;

KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

OS Homo sapiens.

PN WO200259264-A2.

PD 01-AUG-2002.

PF 31-DEC-2001; 2001WO-US049440.

PR 29-DEC-2000; 2000US-00751181.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Hagai Y, Lazarevits J, Guy R, Lipschitz O, Stanton E, Levanon A;

PI Plakshin D, Peretz T;

DR WPI; 2002-619166/66.

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct

PT or fragment, or construct of fragment with enhanced binding

PT characteristics so as to selectively bind target cell in favor of other

PS Claim 4; Page 155-156; 232pp; English.

CC The invention relates to a peptide or polypeptide comprising an Fv

CC molecule, a construct or fragments or a construct of a fragment with

CC enhanced binding characteristics which selectively and/or specifically

CC binds to a target cell in favour of other cells, where binding is

CC primarily determined by a first hypervariable region and Fv is a single

CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in

CC association with or attached, coupled, linked or fused to a

CC pharmaceutical agent, is useful in the manufacture of a medicament, where

CC the medicament has activity against a diseased cell, preferably a cancer

CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,

CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
CC composition for use in inhibiting the growth of a diseased or cancer  
CC cell. This sequence represents a human Fv molecule hypervariable region  
CC related peptide of the invention

XX  
SQ Sequence 277 AA;

Query Match 100.0%; Score 1440; DB 5; Length 277;  
Best Local Similarity 100.0%; Pred. No. 4,5e-89;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLPTAAAGLLLLAQPMAAEVOLVESGGGVRRPGSLRLSCAASGFTPDYGMYSWR 60  
DB 1 MKYLPTAAAGLLLLAQPMAAEVOLVESGGGVRRPGSLRLSCAASGFTPDYGMYSWR 60  
QY 61 QAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRLEDYAVYYCAR 120  
DB 61 QAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRLEDYAVYYCAR 120  
QY 121 MRAPVIMGGTTLTVSRGGSGGGSGGSSSELTQDPAVSVALGQTVRITCGDLSLR 180  
DB 121 MRAPVIMGGTTLTVSRGGSGGGSGGSSSELTQDPAVSVALGQTVRITCGDLSLR 180  
QY 181 YVASWYQOKRGPAPVLYVYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240  
DB 181 YVASWYQOKRGPAPVLYVYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240  
QY 241 RDSGNNHVVFGGSKTLTVLGAAPKLISEEDLNGAA 277  
DB 241 RDSGNNHVVFGGSKTLTVLGAAPKLISEEDLNGAA 277

RESULT 2

ABG91841  
ID ABG91841 standard; protein; 277 AA.

XX AC ABG91841;

XX DT 04-DEC-2002 (first entry)

XX DE Human antibody fragment #25.

XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
XX metastasis; hypervariable region; autoimmune disease; thrombosis;  
XX restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
XX myocardial infarction; retinopathic disease; abnormal platelet function;  
XX sulphated tyrosine-dependent protein-protein interaction.

XX OS Homo sapiens.

XX PN W0200253700-A2.

XX PD 11-JUL-2002.

XX PF 31-DEC-2001; 2001WO-US049442.

XX PR 29-DEC-2000; 2000US-00751181.

XX PR 29-DEC-2000; 2000US-0258948P.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Lazarcovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
XX PI Sanchon E, Richter T, Amit B, Koopertan L, Peretz T, Levanon A;  
XX DR WPI; 2002-674776/72.

XX Novel isolated epitope present on cancer cells and important in  
XX physiological phenomena such as cell rolling, metastasis and  
XX inflammation, for treating autoimmune, inflammatory or cardiovascular  
XX diseases, and cancer.

XX PS Claim 23; Page 233-234; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and  
CC important in physiological phenomena such as cell rolling, metastasis and  
CC inflammation, where the epitope is capable of being bound by an antibody,  
CC its antigen-binding fragment or its complex comprising at least one  
CC antibody or its binding fragment having a first hypervariable region. The  
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
CC mortality of tumour or leukaemia cells, for increasing the susceptibility  
CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
CC leukaemia agents, or for decreasing the number of tumour or leukaemia  
CC cells in a patient, or in the manufacture of a medicament for the above  
CC mentioned purposes. The epitopes are useful for diagnosing and treating  
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
CC diseases, cardiovascular diseases such as myocardial infarction,  
CC retinopathic diseases and other diseases mediated by abnormal platelet  
CC function and diseases caused by sulphated tyrosine-dependent protein-  
CC protein interactions. This sequence represents a human antibody fragment  
CC of the invention

XX  
SQ Sequence 277 AA;

Query Match 100.0%; Score 1440; DB 5; Length 277;  
Best Local Similarity 100.0%; Pred. No. 4,5e-89;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYLPTAAAGLLLLAQPMAAEVOLVESGGGVRRPGSLRLSCAASGFTPDYGMYSWR 60  
DB 1 MKYLPTAAAGLLLLAQPMAAEVOLVESGGGVRRPGSLRLSCAASGFTPDYGMYSWR 60  
QY 61 QAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRLEDYAVYYCAR 120  
DB 61 QAPGKLEWVSGINWNGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRLEDYAVYYCAR 120  
QY 121 MRAPVIMGGTTLTVSRGGSGGGSGGSSSELTQDPAVSVALGQTVRITCGDLSLR 180  
DB 121 MRAPVIMGGTTLTVSRGGSGGGSGGSSSELTQDPAVSVALGQTVRITCGDLSLR 180  
QY 181 YVASWYQOKRGPAPVLYVYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240  
DB 181 YVASWYQOKRGPAPVLYVYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240  
QY 241 RDSGNNHVVFGGSKTLTVLGAAPKLISEEDLNGAA 277  
DB 241 RDSGNNHVVFGGSKTLTVLGAAPKLISEEDLNGAA 277

RESULT 3

AD128366

ID AD128366 standard; protein; 277 AA.

XX AC AD128366;

XX DT 06-MAY-2004 (first entry)

XX DE Human scFv fragment Y1, binds to platelets.

XX Human; antibody; scFv; platelet; drug delivery; cancer; therapy.

XX OS Homo sapiens.

XX PN W02004002528-A1.

XX PD 08-JAN-2004.

XX PF 30-JUN-2003; 2003WO-US020604.

XX PR 01-JUL-2002; 2002US-00189025.

XX PA (SAVI-) SAVIENT PHARM INC.

XX Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;  
 XX MPI; 2004-099189/10.  
 DR  
 XX  
 XX Composition comprising an agent and/or antibody or its fragment, useful  
 PT for treating auto-immune disease, thrombosis, restenosis, metastasis, or  
 PT for inhibiting growth and/or replication of tumor cells or leukemia  
 PT cells.  
 XX  
 PS Claim 13; SEQ ID NO 1, 58pp; English.  
 CC  
 CC The present sequence is the protein sequence of human scFv fragment Y1.  
 CC This antibody was identified by screening a human antibody phage library  
 CC that has diversity only in the heavy chain CDR3 regions. Fixed human  
 CC platelets were screened in order to identify antibodies that bind  
 CC platelets. The epitope for Y1 antibody is located between amino acids 272  
 CC and 285 on glycosylated, a subunit of the CD42 complex. Y1 also binds the  
 CC N-terminal of PEG-1, a receptor for E-, L- and P-selectins, and has a  
 CC high affinity for primary leukemia cells. The invention relates to  
 CC compositions utilising an agent and an antibody or its fragment. The  
 CC agent is a toxin, radioisotope or pharmaceutical agent such as  
 CC doxorubicin. It is complexed or combined with or conjugated to the  
 CC antibody or its fragment. The agent and/or antibody can be present in the  
 CC composition is a sub-clinical amount, i.e. less than the amount generally  
 CC found to be clinically effective when the agent is administered alone.  
 CC The composition is used in claimed methods of: inhibiting cell rolling,  
 CC inflammation, thrombosis, restenosis, metastasis, the growth and/or  
 CC replication of tumor cells or leukemia cells, an increase in number of  
 CC tumor or leukemia cells, cell-cell, cell-matrix, platelet-matrix,  
 CC platelet-platelet and/or cell-platelet complex formation, aggregation or  
 CC adhesion; increasing the mortality rate of tumour or leukemia cells, the  
 CC susceptibility of disease cells to damage by anti-disease agents, and the  
 CC agents; and ameliorating the effects of a disease, preventing a disease,  
 CC treating a disease or inhibiting the progress of a disease.  
 CC  
 XX  
 XX Sequence 277 AA;  
 SQ  
 Query Match 99.7%; Score 1436; DB 8; Length 277;  
 Best Local Similarity 99.6%; Pred. No. 8.4e-89;  
 Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKYLPTAAAGLLLLAOPMAEVLVESGGGVVRRPGSLRLSCAAGFTFDYGMWVR 60  
 DB 1 MKYLPTAAAGLLLLAOPMAEVLVESGGGVVRRPGSLRLSCAAGFTFDYGMWVR 60  
 QY 61 QAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVYYCAR 120  
 DB 61 QAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVYYCAR 120  
 QY 121 MRAPVIMGGTTLTVSRGGSGSGGSSSELTQDPAVSVALGQTVARITCGDSLR 180  
 DB 121 MRAPVIMGGTTLTVSRGGSGSGGSSSELTQDPAVSVALGQTVARITCGDSLR 180  
 QY 181 YVASWYQQRGQAPVLYIKNNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNS 240  
 DB 181 YVASWYQQRGQAPVLYIKNNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNS 240  
 QY 241 RDSSGNHVVFGGSKTLTVGAABEQKLISEEDLNGAA 277  
 DB 241 RDSSGNHVVFGGSKTLTVGAABEQKLISEEDLNGAA 277  
 RESULT 4  
 ABG78328  
 ID ABG78328 standard; protein; 277 AA.  
 XX  
 AC ABG78328;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Human Fv molecule hypervariable region related peptide #203.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytosolic;  
 KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukemia; adenoma;  
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukemia.  
 XX  
 OS Homo sapiens.  
 PN MO200259264-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PE 31-DEC-2001; 2001MO-US049440.  
 XX  
 PR 29-DEC-2000; 2000US-00751181.  
 XX  
 PA (BIO- ) BIO-TECHNOLOGY GEN CORP.  
 PI Hagal Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;  
 PI Plakshin D, Peretz T;  
 XX  
 DR MPI; 2002-619166/66.  
 DR N-PSDB; ABS63384.  
 XX  
 PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 PT or fragment, or construct of fragment with enhanced binding  
 PT characteristic so as to selectively bind target cell in favor of other  
 PT cells.  
 XX  
 PS Claim 14; Fig 14; 232pp; English.  
 XX  
 CC The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukemia cell is an  
 CC acute myeloid leukemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention  
 CC  
 XX  
 XX Sequence 277 AA;  
 SQ  
 Query Match 98.3%; Score 1416; DB 5; Length 277;  
 Best Local Similarity 98.2%; Pred. No. 1.9e-87;  
 Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MKYLPTAAAGLLLLAOPMAEVLVESGGGVVRRPGSLRLSCAAGFTFDYGMWVR 60  
 DB 1 MKYLPTAAAGLLLLAOPMAEVLVESGGGVVRRPGSLRLSCAAGFTFDYGMWVR 60  
 QY 61 QAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVYYCAR 120  
 DB 61 QAPGKLEWVSGINWNGSTGYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVYYCAR 120  
 QY 121 MRAPVIMGGTTLTVSRGGSGSGGSSSELTQDPAVSVALGQTVARITCGDSLR 180  
 DB 121 LTHPYFMGGTTLTVSRGGSGSGGSSSELTQDPAVSVALGQTVARITCGDSLR 180  
 QY 181 YVASWYQQRGQAPVLYIKNNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNS 240  
 DB 181 YVASWYQQRGQAPVLYIKNNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNS 240  
 QY 241 RDSSGNHVVFGGSKTLTVGAABEQKLISEEDLNGAA 277  
 DB 241 RDSSGNHVVFGGSKTLTVGAABEQKLISEEDLNGAA 277



XX	Claim 1; SEQ ID NO 1; 106pp; English.
CC	The present sequence is that of an scFv antibody fragment, designated
CC	L32, that binds P-selectin glycoprotein ligand-1 (PSGL-1). The antibody
CC	was identified by screening a phage library, which had diversity only in
CC	the heavy chain CDR3 regions, against a leukaemia cell to select specific
CC	antibodies that recognised leukaemia cell surface determinants, wherein
CC	the specific receptor was not previously known or characterised. The
CC	invention relates to an antibody or its fragment having the binding
CC	capabilities of L32. Such antibodies can be used in therapeutic,
CC	diagnostic, prognostic and staging methods. Pharmaceutical compositions
CC	comprising such antibodies are used to treat conditions related to:
CC	inhibiting or treating cell rolling, inflammation, autoimmune disease,
CC	infection (e.g. HIV infection), metastasis, and growth and/or replication
CC	of tumour cells; increasing the mortality of tumour cells; inhibiting
CC	growth and/or replication of tumour cells; inhibiting growth and/or
CC	replication of leukaemia cells; increasing the mortality rate of
CC	leukaemia cells; altering the susceptibility of diseased cells to damage
CC	by anti-disease agents; increasing the susceptibility of tumour cells to
CC	damage by anti-cancer agents; increasing the susceptibility of leukaemia
CC	cells to damage by anti-leukaemia agents; inhibiting increase in number
CC	of tumour cells in a patient; decreasing the number of tumour cells in a
CC	patient; inhibiting increase in number of leukaemia cells in a patient;
CC	and decreasing the number of leukaemic cells in a patient. Other methods
CC	are provided to induce antibody-dependent cell-mediated cytotoxicity or
CC	stimulate natural killer or T cells using the antibodies. A method of
CC	pulsing tumour cells from a patient involves incubating the cells with
CC	the antibody.
SQ	Sequence 280 AA:
Query Match	96.8%; Score 1393.5; DB 8; Length 280;
Best Local Similarity	97.1%; Pred. No. 6.1e-86;
Matches 272; Conservative 0; Mismatches 5; Indels 3; Gaps 1;	
OY	1 MKYLPLPAAAGLLILAAQPMAAEVQLVESGGGVYRPGSIRLSCAAGFTPD--DYGMS 57
DB	1 MKYLLPLPAAAGLLILAAQPMAAEVQLVESGGGVYRPGSIRLSCAAGFTPDLPKVM 60
OY	58 WVRQAPKGLEWVSIGIMWGNGSTGYADSVYGRFTISRDNKNLSLYLGMSLRADTAVYY 117
DB	61 WVRQAPKGLEWVSIGIMWGNGSTGYADSVYGRFTISRDNKNLSLYLGMSLRADTAVYY 120
OY	118 CARRAEVLVIWGQITLVTVSRGGSGSGGSGSSSLRTDPAVSVVALGQTIVRTTCGDS 177
DB	121 CARRAEVLVIWGQITLVTVSRGGSGSGGSGGSGSSSLRTDPAVSVVALGQTIVRTTCGDS 180
OY	178 LRSTYSASWYQQKPEQAFLVLIYIGNNPPSGIPDRFGSSSGNTASTLTITGAQAEDADYY 237
DB	181 LRSTYSASWYQQKPEQAFLVLIYIGNNPPSGIPDRFGSSSGNTASTLTITGAQAEDADYY 240
OY	238 CNSRDSSGNHVVRCGGTKTLTVLGAAROKLISEDLNGAA 277
DB	241 CNSRDSSGNHVFEGGTKTLTVLGAAROKLISEDLNGAA 280
RESULT 8	
ADI28368	
ID	ADI28368 standard; protein; 280 AA.
XX	ADI28368;
AC	
DT	06-MAY-2004 (first entry)
XX	
DE	Human scFv fragment L32, binds to leukaemia cells.
XX	
KW	Human; antibody; scFv; leukaemia; drug delivery; cancer; therapy.
OS	Homo sapiens.
XX	
FN	WO2004002528-A1.
XX	

PD 08-JAN-2004.  
 XX  
 PF 30-JUN-2003; 2003WO-US020604.  
 XX  
 PR 01-JUL-2002; 2002US-00189025.  
 XX  
 PA (SAVI-) SAVIENT PHARM INC.  
 XX  
 PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;  
 XX WPI; 2004-099189/10.  
 DR  
 XX Composition comprising an agent and/or antibody or its fragment, useful  
 PT for treating auto-immune disease, thrombosis, restenosis, metastasis, or  
 PT for inhibiting growth and/or replication of tumor cells or leukemia  
 PT cells.  
 XX  
 PS Claim 13; SEQ ID NO 3; 58pp; English.  
 XX  
 CC The present sequence is the protein sequence of human scFv fragment L32.  
 CC This antibody was identified by screening a human antibody phage library  
 CC that has diversity only in the heavy chain CDR3 regions. Leukemia cells  
 CC were screened to select specific antibodies that recognise leukemia cell  
 CC surface determinants. The invention relates to compositions utilising an  
 CC agent and an antibody or its fragment. The agent is a toxin, radioisotope  
 CC or pharmaceutical agent such as doxorubicin. It is complexed or combined  
 CC with or conjugated to the antibody or its fragment. The agent and/or  
 CC antibody can be present in the composition is a sub-clinical amount, i.e.  
 CC less than the amount generally found to be clinically effective when the  
 CC agent is administered alone. The composition is used in claimed methods  
 CC of: inhibiting cell rolling, inflammation, thrombosis, restenosis,  
 CC metastasis, the growth and/or replication of tumor cells or leukemia  
 CC cells, an increase in number of tumor or leukemia cells, cell-cell,  
 CC cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet  
 CC complex formation, aggregation or adhesion; increasing the mortality rate  
 CC of tumor or leukemia cells, the susceptibility of disease cells to  
 CC damage by anti-disease agents, and the susceptibility of tumor or  
 CC leukemia cells to damage by anti-cancer agents; and ameliorating the  
 CC effects of a disease, preventing a disease, treating a disease or  
 CC inhibiting the progress of a disease.  
 XX  
 SQ Sequence 280 AA;  
 Query Match 96.3%; Score 1386.5; DB 8; Length 280;  
 Best Local Similarity 96.8%; Pred. No. 1.8e-85;  
 Matches 271; Conservative 0; Mismatches 6; Indels 3; Gaps 1;  
 QY 1 MKTLLPTAAAGLLILAAQPMMAEVQVLESQGVVRRPGSGIRLSCASGFTFDY--DYGMS 57  
 DB 1 MKTLLPTAAAGLLILAAQPMMAEVQVLESQGVVRRPGSGIRLSCASGFTFDY--DYGMS 60  
 QY 58 WVAQAPGKGLWVSGINWNGSGTGYADSVKGRFTISRDNAKNSLYIQOMSLRAEDTAVVY 117  
 DB 61 WVAQAPGKGLWVSGINWNGSGTGYADSVKGRFTISRDNAKNSLYIQOMSLRAEDTAVVY 120  
 QY 118 CARMRAPIVINGQGLTVIVSRGGSGGSGGSSSLTQDPNAVVALGQTVIRITCGGDS 177  
 DB 121 CARMRAPIVINGQGLTVIVSRGGSGGSGGSSSLTQDPNAVVALGQTVIRITCGGDS 180  
 QY 178 LRSYVASWYQKPGQAPFVLVIYGNKRRPSGI PDRFSSSSSGNTASLTITTAQAEDADYY 237  
 DB 181 LRSYVASWYQKPGQAPFVLVIYGNKRRPSGI PDRFSSSSSGNTASLTITTAQAEDADYY 240  
 QY 238 CNSRDSGSGNHVVRGGGKTKTVLGAFAEOKLISEEDLNGAA 277  
 DB 241 CNSRDSGSGNHVVRGGGKTKTVLGAFAEOKLISEEDLNGAA 280

XX  
 DT 04-DEC-2002 (first entry)  
 XX  
 DE Human antibody fragment #204.  
 XX  
 KW Human; antibody; epitope; cancer; tumor; cell rolling; inflammation;  
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;  
 KW restenosis; leukemia; inflammatory disease; cardiovascular disease;  
 KW myocardial infarction; retinopathic disease; abnormal platelet function;  
 KW sulphated tyrosine-dependent protein-protein interaction.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200253700-A2.  
 XX  
 PD 11-JUL-2002.  
 XX  
 PF 31-DEC-2001; 2001WO-US049442.  
 XX  
 PR 29-DEC-2000; 2000US-00751181.  
 PR 29-DEC-2000; 2000US-0258948P.  
 XX  
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 XX  
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
 PI Szanthon E, Richter T, Amit B, Koepman L, Peretz T, Levanon A;  
 XX WPI; 2002-674776/72.  
 DR  
 XX Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer.  
 XX  
 PS Disclosure; Page 309-310; opp; English.  
 XX  
 CC The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
 CC tumor or leukemia cells, increase in number of tumor or leukemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
 CC mortality of tumor or leukemia cells, for increasing the susceptibility  
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
 CC leukemia agents, or for decreasing the number of tumor or leukemia  
 CC cells in a patient, or in the manufacture of a medicament for the above  
 CC mentioned purposes. The epitopes are useful for diagnosing and treating  
 CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory  
 CC diseases, cardiovascular diseases such as myocardial infarction,  
 CC retinopathic diseases and other diseases mediated by abnormal platelet  
 CC function and diseases caused by sulphated tyrosine-dependent protein-  
 CC protein interactions. This sequence represents a human antibody fragment  
 CC of the invention  
 XX  
 SQ Sequence 266 AA;  
 Query Match 95.7%; Score 1378; DB 5; Length 266;  
 Best Local Similarity 99.2%; Pred. No. 6.4e-85;  
 Matches 264; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKTLLPTAAAGLLILAAQPMMAEVQVLESQGVVRRPGSGIRLSCASGFTFDYGMWVR 60  
 DB 1 MKTLLPTAAAGLLILAAQPMMAEVQVLESQGVVRRPGSGIRLSCASGFTFDYGMWVR 60  
 QY 61 QAPGKGLWVSGINWNGSGTGYADSVKGRFTISRDNAKNSLYIQOMSLRAEDTAVVYCAR 120  
 DB 61 QAPGKGLWVSGINWNGSGTGYADSVKGRFTISRDNAKNSLYIQOMSLRAEDTAVVYCAR 120  
 QY 121 MRAPVINGQGLTVIVSRGGSGGSGGSSSLTQDPNAVVALGQTVIRITCGGDSLRS 180



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Db      121  MRAPVINGQGLTVVSRGGGSGGSGGSSSELTQDPAPVVALGQTVRITCGGSLRS 180
Qy      181  YVASWYQKQKQAPVLYVYGNKNNRPSGIPDRFGSSSGNTASLTITGAQADEADYYCNS 240
Db      181  YVASWYQKQKQAPVLYVYGNKNNRPSGIPDRFGSSSGNTASLTITGAQADEADYYCNS 240
Qy      241  RDSSGNHVFEGGKTKLTVLGAABEQK 266
Db      241  RDSSGNHVFEGGKTKLTVLGAABAKAK 266

RESULT 10
ADN06989  standard; protein; 291 AA.
AC      ADN06989;
AD      01-JUL-2004 (first entry)
DE      Human EGFR bs-scfv antibody protein, HER3.B12.
KW      Bispecific single chain; bs-scfv; cancer;
KW      epidermal growth factor receptor; EGFR; therapy; antibody; human.
OS      Homo sapiens.
XX      US2004071696-A1.
XX      15-APR-2004.
XX      04-APR-2003; 2003US-00406830.
XX      05-APR-2002; 2002US-0370276P.
PA      (REGC-) UNIV CALIFORNIA.
PA      (FOXC-) FOX CHASE CANCER CENT.
PI      Adams GP, Horak EM, Weiner LM, Marks JD;
XX      WPI; 2004-328525/30.
XX      Novel bispecific antibody comprising first and second antibody joined to
XX      each other and having binding specificity to different epitopes of
XX      Epidermal Growth Factor Receptor protein, useful for treating cancer.
PS      Claim 14; SEQ ID NO 6; 57bp; English.
XX      The present invention provides bispecific single chain (bs-scfv) antibody
XX      molecules which may be used to treat various forms of cancer associated
XX      with the overexpression of the epidermal growth factor receptor (EGFR)
XX      family. The invention is useful for specifically delivering an effector
XX      molecule to a cell bearing a receptor from EGFR protein family chosen
XX      from EGFR, HER2/neu, HER3 and HER4. The invention is useful in the
XX      treatment of cancer. The present sequence is human EGFR bs-scfv antibody
XX      protein.
SQ      Sequence 291 AA;

Query Match      89.9%; Score 1294; DB 8; Length 291;
Best Local Similarity 88.8%; Pred. No. 3.2e-79;
Matches 253; Conservative 10; Mismatches 14; Indels 8; Gaps 2;
Qy      1  MKTLLPRAAGLLILAAQPMAYEVQVLSGGGVYRPGGSLRLSCAASGFTPDYGMQSWR 60
Db      1  MKTLLPRAAGLLILAAQPMAYEVQVLSGGGVYRPGGSLRLSCAASGFTPDYGMQSWR 60
Qy      61  QADGKGLWYSGINMGSGTGVADSVKGRFTISRDNAKNSLYIQMNSLRAPEDYAVYYCAR 120
Db      61  QADGKGLWYSGINMGSGTGVADSVKGRFTISRDNAKNSLYIQMNSLRAPEDYAVYYCAR 120
Qy      121  -----MRAPVINGQGLTVVSRGGGSGGSGGSS-ELTQDPAPVVALGQTVRIT 172

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```

Db      121  DLGAKQWLEBFDYWGQGLTVVSRGGGSGGSGGSSNFMLTQDPAPVVALGQTVRIT 180
Qy      173  CGDPSLRSYYASWYQKQKQAPVLYVYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAD 232
Db      181  CGDPSLRSYYASWYQKQKQAPVLYVYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAD 240
Qy      233  EADYYCNSRDSGNNHVFEGGKTKLTVLGAABEQKLTISEEDLNGAA 277
Db      241  EADYYCNSRDSGNNHVFEGGKTKLTVLGAABEQKLTISEEDLNGAA 285

RESULT 11
AAE02185  standard; protein; 282 AA.
ID      AAE02185;
AC      AAE02185;
AD      10-AUG-2001 (first entry)
DE      PAM1 single chain variable region (scfv) antibody.
KW      Pectin; PAM1 antibody; single chain variable region; scfv; food; jam;
KW      yogurt; gel; homogalacturonan; HG; plant cell wall.
OS      Unidentified.
XX      Key
XX      Location/Qualifiers
XX      1..22
XX      Peptide
XX      /label= pelB_leader_sequence
XX      23..140
XX      Region
XX      /label= Heavy_chain_fragment
XX      141..156
XX      Region
XX      /label= linker
XX      157..277
XX      Region
XX      /label= light_chain_fragment
XX      267..277
XX      Region
XX      /label= Myc_epitope
XX      Misc-difference 277..282
XX      /note= "Encoded by AAT"

US6228599-B1.
08-MAY-2001.
26-FEB-1999; 99US-00260527.
24-DEC-1998; 98GB-00028700.
PA      (DANI-) DANISCO AS.
PI      Knox JP, Willats WGT, Mikkelsen JD;
XX      WPI; 2001-342672/36.
XX      N-PSDB; AAD06193.
XX      New PAM1 and PAM2 antibodies capable of binding de-esterified
XX      homogalacturonan, useful for identifying a pectin moiety, for quantifying
XX      the amount of pectin in a sample or for extracting pectin from a sample.
XX      Claim 1; Fig 4B; 21bp; English.
XX      The invention relates to antibodies specific to pectin, such as PAM1 and
XX      PAM2 scfv (single chain variable region). These antibodies are derived
XX      from a naive phage display library known as the synthetic scfv library
XX      (#1). PAM1 and PAM2 antibodies are capable of binding to de-esterified
XX      and un-substituted homogalacturonan (HG), useful for identifying a pectin
XX      motif. PAM antibody is useful for identifying a pectin functional group
XX      and in assays to determine if a particular pectin composition has the
XX      pectin motif or can be used to prepare a food for human and animal
XX      consumption, such as jams, yogurts or gels. The PAM antibodies are
XX      further useful for quantifying the amount of pectin in a sample or for
XX      extracting pectin from a sample. PAM antibodies are also used to identify
XX      de-esterified homogalacturonan blocks in the primary cell walls of

```

CC plants. The present sequence is PAM1 scfv antibody specific to pectin.  
 CC Note: This sequence is stated as being the same as that shown as SEQ ID  
 CC NO: 1 in the sequence listing of the specification, however the sequence  
 CC has 2 extra residues at the C-terminal end

XX Sequence 282 AA;

Query Match 88.8%; Score 1278.5; DB 4; Length 282;  
 Best Local Similarity 90.0%; Pred. No. 3,4e-78;  
 Matches 253; Conservative 10; Mismatches 15; Indels 3; Gaps 2;

QY 1 MKYLLPTAAAGLLLLAQPMAAEVOLVESGGGVVRPGGSLRLSCAASGFTEDDYGMWVR 60  
 DB 1 MKYLLPTAAAGLLLLAQPMAAEVOLVESGGGVVRPGGSLRLSCAASGFTESNMMWVR 60  
 QY 61 QAGKGIEMWVSGI--MNAGSGTGYADSVKRFITSPNANNSLYLQNSLRADDTAVYVC 118  
 DB 61 QAGKGIEMWVSGI--MNAGSGTGYADSVKRFITSPNANNSLYLQNSLRADDTAVYVC 120  
 QY 119 AR-MRAPVINGGGLTVTVSRGGSGGGGSSSELTPDPAVSVALGQTVRITCGDS 177  
 DB 121 ARKMRKRLRMGGGLTVTVSRGGSGGGGSSSELTPDPAVSVALGQTVRITCGDS 180  
 QY 178 LRSYVASWYQKPGQAPFVLYYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDADYY 237  
 DB 181 LRSYVASWYQKPGQAPFVLYYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDADYY 240  
 QY 238 CNSRDSGGNHVVFSGGKTLTVLGAAMQKLISEEDLNGAA 277  
 DB 241 CNSRDSGGNHVVFSGGKTLTVLGAAMQKLISEEDLNGAA 280

#### RESULT 12

AAW83322 ID AAW83322 standard; protein; 309 AA.

AC AAW83322;

DT 16-MAR-1999 (first entry)

XX Single chain Apo-2 antibody 16E2.

XX Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;  
 KM tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;  
 KM TNF cytokine.

OS Homo sapiens.

XX NC9851793-A1.

PD 19-NOV-1998.

PF 14-MAY-1998; 98WC-US009704.

XX 15-MAY-1997; 97US-00857216.

PR 09-FEB-1998; 98US-00020746.

XX (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Adams CW, Chuntharapai A, Kim KI;

DR WPI; 1999-045228/04.

DR N-PSDB; AAV72532.

XX Human Apo-2 polypeptide inducing apoptosis - useful to treat conditions  
 PT linked with decreased apoptosis e.g. cancer, and produce antibodies to  
 PT increase or decrease apoptosis.

XX Example 14; Fig 16; 134pp; English.

CC The present invention describes human Apo-2. Apo-2 can be used  
 CC therapeutically to induce apoptosis in mammalian cells, and so is useful  
 CC to treat conditions associated with decreased apoptosis e.g. cancer. Apo-

CC 2 is believed to be a new tumour necrosis factor (TNF) receptor (TNFR).  
 CC TNF cytokines can induce apoptosis, thought to be initiated by binding to  
 CC TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It can be used to  
 CC identify agents activating Apo-2, useful to treat mammalian cancer cells,  
 CC and to produce Apo-2 chimeras useful therapeutically (e.g. those  
 CC containing immunoglobulin sequences can be inhibit apoptosis) or  
 CC diagnostically (e.g. those comprising an epitope tag polypeptide allow  
 CC Apo-2 detection and purification using anti-tag antibodies). It can be  
 CC used to produce antibodies which can be combined with a (particularly  
 CC pharmaceutically acceptable) carrier in compositions or used to produce  
 CC dimeric molecules (especially homodimeric molecules comprising first and  
 CC second Apo-2 antibodies). Agonistic (especially single-chain) antibodies  
 CC can be administered to induce apoptosis in mammalian cancer cells, and  
 CC antagonistic antibodies used to block excessive apoptosis (e.g. in  
 CC neurodegenerative diseases). Apo-2 antibodies may also be used  
 CC diagnostically e.g. to detect Apo-2 expression in cells/tissues and in  
 CC Apo-2 purification. The present sequence represents a single chain Apo-2  
 CC antibody, designated 16E2

XX Sequence 309 AA;

Query Match 88.6%; Score 1275.5; DB 2; Length 309;  
 Best Local Similarity 89.9%; Pred. No. 5.9e-78;  
 Matches 249; Conservative 5; Mismatches 8; Indels 15; Gaps 2;

QY 16 AQPMAAEVOLVESGGGVVRPGGSLRLSCAASGFTEDDYGMWVRQAPGKLEWVSGINW 75  
 DB 33 AQPMAAEVOLVOSGGGVVRPGGSLRLSCAASGFTEDDYGMWVRQAPGKLEWVSGINW 92  
 QY 76 NGSGTGYADSVKRFITSPNANNSLYLQNSLRADDTAVYCARNRAP-----VINGQ 129  
 DB 93 NGSGTGYADSVKRFITSPNANNSLYLQNSLRADDTAVYCARNRAP-----VINGQ 152  
 QY 130 GTLVTVSRGGSGGGGSSSELTPDPAVSVALGQTVRITCGDSLSRYASWYQOK 189  
 DB 153 GTLVTVSRGGSGGGGSSSELTPDPAVSVALGQTVRITCGDSLSRYASWYQOK 212  
 QY 190 PGQAPVLYYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDADYYCNSRDSGGNHV 249  
 DB 213 PGQAPVLYYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDADYYCNSRDSGGNHV 272  
 QY 250 FGGGTTLTVLGA-----AAEQKLISEEDLNGAA 277  
 DB 273 FGGGTTLTVLGAHHHHHGALEQKLISEEDLNGAA 309

#### RESULT 13

ABB09603 ID ABB09603 standard; protein; 309 AA.

AC ABB09603;

DT 29-MAY-2002 (first entry)

XX Amino acid sequence of single-chain Apo-2 antibody 16E2.

XX Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis; caspase;  
 KM apoptosis; cancer; antibody.

OS Bacteriophage.

XX US6342369-B1.

PD 29-JAN-2002.

PF 14-MAY-1998; 98US-00079029.

XX 15-MAY-1997; 97US-0046615P.

PR 09-FEB-1998; 98US-0074119P.

XX (GETH ) GENENTECH INC.

PI Ashkenazi AJ;

XX WPI; 2002-224941/28.  
 DR N-PSDB; ABL41733.  
 XX  
 PT New nucleic acids encoding an Apo-2 ligand, useful for activating or  
 PT stimulating apoptosis in cancer cells, thus especially useful in the  
 PT treatment of cancer, or in enhancing immune-mediated cell death.  
 XX  
 XX Example 14; Fig 16; 68pp; English.  
 PS  
 CC The present sequence represents a single-chain Apo-2 antibody, designated  
 CC 16E2, which is isolated from a phage library. It is believed that Apo-2  
 CC is a member of the tumour necrosis factor receptor (TNFR) family. Apo-2  
 CC polypeptide is capable of triggering caspase-dependent apoptosis and  
 CC activating nuclear factor-kappa B. A soluble extracellular domain of Apo-  
 CC 2 binds Apo-2 ligand (Apo-2L). Apo-2 antibodies may be used to activate  
 CC or stimulate apoptosis in cancer cells. They are therefore especially  
 CC useful in the treatment of cancer, to enhance immune-mediated cell death  
 CC in cells expressing Apo-2, to detect expression of Apo-2 in specific  
 CC cells, tissues or serum, and in affinity purification of Apo-2 from  
 CC recombinant cell culture or natural sources  
 CC  
 XX Sequence 309 AA;  
 SQ  
 Query Match 88.6%; Score 1275.5; DB 5; Length 309;  
 Best Local Similarity 89.9%; Pred. No. 5.9e-78;  
 Matches 249; Conservative 5; Mismatches 8; Indels 15; Gaps 2;  
 QY 16 AADPAAAEVOLVESGGGVPRGSLRLSCAAGFTPDYGMVVRQAPGKLEWVGINW 75  
 DB 33 AADPAAAEVOLVOSGGGVPRGSLRLSCAAGFTPDYGMVVRQAPGKLEWVGINW 92  
 QY 76 NGSGTAVSVKRFRTISRDNANKSLYLQNNSLRAEDTAVYYCARMRAP-----VIMQ 129  
 DB 93 NGSGTAVSVKRFRTISRDNANKSLYLQNNSLRAEDTAVYYCARMRAP-----VIMQ 152  
 QY 130 GTLVTVSRGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCQGDLSLSYASWYQOK 189  
 DB 153 GTLVTVSRGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCQGDLSLSYASWYQOK 212  
 QY 190 PGQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHV 249  
 DB 213 PGQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHV 272  
 QY 250 FGGGTKLTVLGA-----AAEQKLISEEDLNGAA 277  
 DB 273 FGGGTKLTVLGAAGAAHHHHHGAAGQKLISEEDLNGAA 309

RESULT 14  
 ABG74384  
 ID ABG74384 standard; protein; 309 AA.  
 AC  
 XX ABG74384;  
 XX  
 DT 11-APR-2003 (first entry)  
 XX  
 DE Single chain antibody (scFv) fragment 16E2.  
 XX  
 KW Apo-2; tumour necrosis factor family; TNFR; gene therapy; apoptosis;  
 KW tissue-specific typing; affinity purification;  
 KW competitive-type receptor binding assay; mouse; 16E2.  
 XX  
 OS Mus sp.  
 XX  
 PN US2002150985-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 02-NOV-2001; 2001US-00052798.  
 XX  
 PR 15-MAY-1997; 97US-0046615P.  
 PR 09-FEB-1998; 98US-0074119P.

PR 14-MAY-1998; 98US-00079029.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;  
 XX  
 DR WPI; 2003-198287/19.  
 DR N-PSDB; ABX16407.  
 XX  
 PT New Apo-2 polypeptides and polynucleotides, useful for inducing apoptosis  
 PT in mammalian cells, in vivo or ex vivo gene therapy, in quantitative  
 PT diagnostic assays, or in generating antibodies against Apo-2.  
 XX  
 XX Example 14; Fig 16; 64pp; English.  
 PS  
 CC The invention describes a novel isolated Apo-2 polypeptide. The Apo-2  
 CC polypeptide is useful for inducing apoptosis in mammalian cells, in vivo  
 CC or ex vivo gene therapy, in quantitative diagnostic assays, as a control  
 CC against samples containing unknown quantities of Apo-2, in generating  
 CC antibodies, in affinity purification techniques, and in competitive-type  
 CC receptor binding assays when labelled with, for instance, radioiodine,  
 CC enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a  
 CC diagnostic for tissue-specific typing. This is the amino acid sequence of  
 CC the single chain antibody fragment (svFv) 16E2 used in the preparation of  
 CC anti-apo-2 antibodies  
 CC  
 XX Sequence 309 AA;  
 SQ  
 Query Match 88.6%; Score 1275.5; DB 6; Length 309;  
 Best Local Similarity 89.9%; Pred. No. 5.9e-78;  
 Matches 249; Conservative 5; Mismatches 8; Indels 15; Gaps 2;  
 QY 16 AADPAAAEVOLVESGGGVPRGSLRLSCAAGFTPDYGMVVRQAPGKLEWVGINW 75  
 DB 33 AADPAAAEVOLVOSGGGVPRGSLRLSCAAGFTPDYGMVVRQAPGKLEWVGINW 92  
 QY 76 NGSGTAVSVKRFRTISRDNANKSLYLQNNSLRAEDTAVYYCARMRAP-----VIMQ 129  
 DB 93 NGSGTAVSVKRFRTISRDNANKSLYLQNNSLRAEDTAVYYCARMRAP-----VIMQ 152  
 QY 130 GTLVTVSRGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCQGDLSLSYASWYQOK 189  
 DB 153 GTLVTVSRGGGSGGGGSGGSSSELTQDPAVSVALGQTVRITCQGDLSLSYASWYQOK 212  
 QY 190 PGQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHV 249  
 DB 213 PGQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHV 272  
 QY 250 FGGGTKLTVLGA-----AAEQKLISEEDLNGAA 277  
 DB 273 FGGGTKLTVLGAAGAAHHHHHGAAGQKLISEEDLNGAA 309

RESULT 15  
 ADG98737  
 ID ADG98737 standard; protein; 309 AA.  
 AC  
 XX ADG98737;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Human single chain antibody (scFv) 16E2 protein.  
 XX  
 KW Apo-2; apoptosis; diagnosis; tissue-specific typing; transgenic animal;  
 KW cancer; gene therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key  
 FT Peptide  
 FT  
 FT 1. .12  
 FT /label= Signal\_peptide  
 FT 13. .309  
 FT /note= "Human mature single chain antibody protein"

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FT /note= "heavy chain complementarity determining region 1"
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FT /note= "heavy chain CDR2"
FT /note= "heavy chain complementarity determining region 2"
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FT /note= "heavy chain complementarity determining region 3"
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FT /note= "light chain CDR3"
FT /note= "light chain complementarity determining region 3"
PN US2003148455-A1.
XX
XX 07-AUG-2003.
XX
XX 06-NOV-2002; 2002US-00288917.
XX
XX 15-MAY-1997; 97US-0046615P.
XX 09-FEB-1998; 98US-0074119P.
XX 14-MAY-1998; 98US-00079029.
XX 02-NOV-2001; 2001US-00052798.
XX
XX (GETH ) GENENTECH INC.
XX
XX PI Adams CW, Ashkenazi AJ, Chuntarapai A, Kim KJ;
XX DR WPI; 2003-897574/82.
XX DR N-PSDB; ADG98734.
XX
XX PT New Apo-2 polypeptide or its extracellular or death domain sequence,
XX PT useful for modulating apoptosis in mammalian cancer cells or for
XX PT generating transgenic or knockout animals.
XX
XX PS Example 14; SEQ ID NO 9; 64pp; English.
XX
XX CC The present invention provides novel Apo-2 protein and the nucleic acid
XX CC encoding the protein. The invention is useful in inducing apoptosis in
XX CC mammalian cancer cells. The invention is also useful in diagnostic
XX CC procedures for tissue-specific typing and in generating transgenic
XX CC animals that are useful in development and in screening of reagents. The
XX CC invention is also useful in gene therapy. The present sequence is human
XX CC single chain antibody (scfv) protein.
XX
XX SQ Sequence 309 AA;
XX
XX Query Match 88.6%; Score 1275.5; DB 7; Length 309;
XX Best Local Similarity 89.9%; Pred. No. 5.9e-78;
XX Matches 249; Conservative 5; Mismatches 8; Indels 15; Gaps 2;
QY 16 AAQPMAMEVQLVESGGGVVPRGSLRLSCAASGFTPDYGMKSWTRQAPGKLEWVSGINW 75
DB 33 AAQPMAMEVQLVDSGGVPRGSLRLSCAASGFTPDYGMKSWTRQAPGKLEWVSGINW 92
QY 76 NGGSTGADSVKGRFTISRDNAKNSLYLQNNSLRAEDTAVYYCARMRAP-----VIWGQ 129
DB 93 NGGSTGADSVKGRFTISRDNAKNSLYLQNNSLRAEDTAVYYCAKITGAGRGWTFDLMGK 152
QY 130 GTLVTVSRGGGGSGGGSGGGSSSELTQDPAVSVVALGQTVRITQGDLSRSYASWYQOK 189
DB 153 GTLVTVSRGGGGSGGGSGGGSSSELTQDPAVSVVALGQTVRITQGDLSRSYASWYQOK 212
QY 190 PGQAPVLVITYGKNNRPSGIPRFSGSSSGNTASLITIGQAQEDADYTCNSRDSGNHVV 249
DB 213 PGQAPVLVITYGKNNRPSGIPRFSGSSSGNTASLITIGQAQEDADYTCNSRDSGNHVV 272
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QY 250 FGGGTCLTVLGA-----AAEQKLISEEDLNGAA 277
DB 273 FGGGTCLTVLGAHHHHHHHGAEEQKLISEEDLNGAA 309
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:24:31 ; Search time 42.6863 Seconds  
(without alignments)  
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Perfect score: 1440

Sequence: 1 MKYLLPTAAAGLLLAQAQA.....VLGAARQKLISEEDINGAA 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 513545

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: Issued Patents AA:\*  
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3: /cgn2\_6/prodata/1/aa/5B COMB pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1278.5	88.8	280	US-09-260-527-1	Sequence 1, Appl
2	1275.5	88.6	309	US-09-079-029-9	Sequence 9, Appl
3	1194	82.9	312	US-09-079-029-10	Sequence 10, Appl
4	1126.5	78.2	278	US-09-260-527-3	Sequence 3, Appl
5	973	67.6	310	US-09-079-029-11	Sequence 11, Appl
6	836.5	58.1	284	US-08-564-164A-2	Sequence 2, Appl
7	829	57.6	282	US-08-860-174A-10	Sequence 10, Appl
8	822	57.1	268	US-09-976-118-1	Sequence 1, Appl
9	803	55.8	240	US-09-192-854-2	Sequence 2, Appl
10	800	55.6	289	US-09-184-658-63	Sequence 63, Appl
11	800	55.6	289	US-09-504-262D-63	Sequence 63, Appl
12	797.5	55.4	334	US-09-646-028-53	Sequence 53, Appl
13	797.5	55.4	339	US-09-646-028-55	Sequence 55, Appl
14	791.5	55.0	348	US-09-646-028-51	Sequence 51, Appl
15	787.5	54.7	245	US-08-918-148-75	Sequence 75, Appl
16	787.5	54.7	245	US-09-138-091A-73	Sequence 73, Appl
17	786.5	54.6	245	US-08-918-148-76	Sequence 76, Appl
18	786.5	54.6	245	US-09-138-091A-74	Sequence 74, Appl
19	786	54.6	255	US-09-553-498-8	Sequence 8, Appl
20	786	54.6	255	US-09-618-869-8	Sequence 8, Appl
21	781.5	54.3	245	US-08-918-148-78	Sequence 78, Appl
22	781.5	54.3	245	US-09-138-091A-76	Sequence 76, Appl
23	775	53.8	272	US-09-726-219A-183	Sequence 183, Appl
24	772.5	53.6	301	US-08-661-052-14	Sequence 14, Appl
25	772.5	53.6	301	US-09-188-082-14	Sequence 14, Appl
26	772.5	53.6	301	US-09-364-088-14	Sequence 14, Appl
27	772.5	53.6	301	US-09-102-716-14	Sequence 14, Appl

28	761	52.8	281	3	US-09-025-769B-178	Sequence 178, App
29	761	52.8	281	4	US-09-490-070A-178	Sequence 178, App
30	761	52.8	281	4	US-09-490-153-178	Sequence 178, App
31	761	52.8	281	4	US-09-490-324-178	Sequence 178, App
32	758	52.6	288	3	US-09-423-439-38	Sequence 38, Appl
33	757	52.6	244	3	US-08-918-148-77	Sequence 77, Appl
34	757	52.6	244	4	US-09-138-091A-75	Sequence 75, Appl
35	745.5	51.8	267	3	US-09-485-737B-2	Sequence 2, Appl
36	745.5	51.8	267	4	US-10-071-985-2	Sequence 2, Appl
37	744.5	51.7	402	2	US-08-491-988-9	Sequence 9, Appl
38	742.5	51.6	281	3	US-09-423-439-44	Sequence 44, Appl
39	739.5	51.4	415	2	US-08-491-988-7	Sequence 7, Appl
40	739.5	51.4	435	2	US-08-491-988-5	Sequence 5, Appl
41	737.5	51.2	269	2	US-08-428-257A-72	Sequence 72, Appl
42	737.5	51.2	269	2	US-08-491-988-3	Sequence 3, Appl
43	737	51.2	359	4	US-09-646-028-16	Sequence 16, Appl
44	731	50.8	265	2	US-08-403-853-16	Sequence 16, Appl
45	731	50.8	361	4	US-09-646-028-13	Sequence 13, Appl

#### ALIGNMENTS

RESULT 1  
US-09-260-527-1

Sequence 1, Application US/09260527A

Patent No. 6228599

GENERAL INFORMATION:

APPLICANT: Knox, J.P.

APPLICANT: Mikelsen, J.D.

APPLICANT: Willats, W. G.

TITLE OF INVENTION: ANTIBODY

FILE REFERENCE: DYO019.001AUS

CURRENT APPLICATION NUMBER: US/09/260,527A

CURRENT FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1

LENGTH: 280

TYPE: PRT

ORGANISM: UNKNOWN

FEATURE:

OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a

OTHER INFORMATION: phase display library known as the Synthetic scFv

OTHER INFORMATION: Library (#1) from the Centre for Protein

OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.

US-09-260-527-1

Query Match 88.8%; Score 1278.5; DB 3; Length 280;

Best Local Similarity 90.0%; Pred. No. 1.9e-95;

Matches 252; Conservative 10; Mismatches 15; Indels 3; Gaps 2;

QY	1	MKYLLPTAAAGLLLAQAQA.....VLGAARQKLISEEDINGAA 277	60
DB	1	MKYLLPTAAAGLLLAQAQA.....VLGAARQKLISEEDINGAA 280	60
QY	61	QAPGKLEAVSGI--NMNGSGTGYADSVYGRFTISDNANQSLYLQMSIRADTVAYYC 118	
DB	61	QAPGKLEAVSGI--NMNGSGTGYADSVYGRFTISDNANQSLYLQMSIRADTVAYYC 120	
QY	119	AR-MRAPVIMGGTTLTVTSRGGSGGSGGSSSELTPDPVSVALGQTVAITCGDS 177	
DB	121	ARKMRPALMGGTTLTVTSRGGSGGSGGSSSELTPDPVSVALGQTVAITCGDS 180	
QY	178	LRSYASWTQOKRGQAPVIVIGKNNRPSGIDPFRSGSSSGNTASLTITGAQAEADYV 237	
DB	181	LRSYASWTQOKRGQAPVIVIGKNNRPSGIDPFRSGSSSGNTASLTITGAQAEADYV 240	
QY	238	CNSRDSGHHVVFGGGTGKTLTVGAARQKLISEEDINGAA 277	
DB	241	CNSRDSGHHVVFGGGTGKTLTVGAARQKLISEEDINGAA 280	

```
RESULT 2
US-09-079-029-9
; Sequence 9, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-9

Query Match      88.6%; Score 1275.5; DB 3; Length 309;
Best Local Similarity 89.9%; Pred. No. 3.7e-95;
Matches 249; Conservative 5; Mismatches 8; Indels 15; Gaps 2;

QY 16 AAQPAAAEVQLVDSGGGVRRPGSLRLSCAASGFTFDYGMWVRAQPGKLEWVSGINW 75
DB 33 AAQPAAAEVQLVDSGGGVRRPGSLRLSCAASGFTFDYGMWVRAQPGKLEWVSGINW 92
QY 76 NGSTGYADSVKGRFTISRDNKNSLYLQWNSLRADDTAVYYCARMRAP-----VTWGQ 129
DB 93 NGSTGYADSVKGRFTISRDNKNSLYLQWNSLRADDTAVYYCARMRAP-----VTWGQ 152
QY 130 GTLVTVSRGGGGSGGGSGGGSSSELTQDPAVSVALGQTVRITCGDLSLSYYASWYQOK 189
DB 153 GTLVTVSRGGGGSGGGSGGGSSSELTQDPAVSVALGQTVRITCGDLSLSYYASWYQOK 212
QY 190 PGQAPVLYVYIGKNNRPFGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHV 249
DB 213 PGQAPVLYVYIGKNNRPFGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHV 272
QY 250 FGGGTLTVLGA-----AAEQKLISEEDLNGAA 277
DB 273 FGGGTLTVLGA-----AAEQKLISEEDLNGAA 309

RESULT 3
US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
```

```
APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-10

Query Match      82.9%; Score 1194; DB 3; Length 312;
Best Local Similarity 85.0%; Pred. No. 1.4e-88;
Matches 238; Conservative 5; Mismatches 19; Indels 18; Gaps 2;

QY 16 AAQPAAAEVQLVDSGGGVRRPGSLRLSCAASGFTFDYGMWVRAQPGKLEWVSGINW 75
DB 33 AAQPAAAEVQLVDSGGGVRRPGSLRLSCAASGFTFDYGMWVRAQPGKLEWVSGINW 92
QY 76 NGSTGYADSVKGRFTISRDNKNSLYLQWNSLRADDTAVYYCARMRAP-----I 126
DB 93 DGEKTYVDSVKGRFTISRDNKNSLYLQWNSLRADDTAVYYCARMRAP-----I 152
QY 127 WGGTLYTVSRGGGGSGGGSGGGSSSELTQDPAVSVALGQTVRITCGDLSLSYYASWY 186
DB 153 WGGTLYTVSRGGGGSGGGSGGGSSSELTQDPAVSVALGQTVRITCGDLSLSYYASWY 212
QY 187 QOKPGAPVLYVYIGKNNRPFGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGN 246
DB 213 QOKPGAPVLYVYIGKNNRPFGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGN 272
QY 247 HVFVGGGTLTVLGA-----AAEQKLISEEDLNGAA 277
DB 273 HVFVGGGTLTVLGA-----AAEQKLISEEDLNGAA 312

RESULT 4
US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelson, J.D.
; APPLICANT: Willate, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
```

SEQ ID NO 3  
LENGTH: 278  
TYPE: PRT  
ORGANISM: UNKNOWN  
FEATURE:  
OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected  
OTHER INFORMATION: from a naive phage display library known as the  
OTHER INFORMATION: Synthetic scfv library (#1) from the Centre for  
OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK  
US-09-260-527-3

Query Match 78.2%; Score 1126.5; DB 3; Length 278;  
Best Local Similarity 80.3%; Pred. No. 3.3e-83;  
Matches 224; Conservative 17; Mismatches 35; Indels 3; Gaps 3;

QY 1 MKTLPAAAGLLILAAQPMABEVQVSGGGGVRPGGSLRLSCAAGFTPDYDYG-MSW 59  
DB 1 MKTLPAAAGLLILAAQPMABEVQVSGGGGVRPGGSLRLSCAAGFTPDYDYG-MSW 60  
QY 60 ROAPGKLEWVSGINMGSTGYADVGRFTISRDNKNSLYLQNNSLRAEDTAVYYCA 119  
DB 61 RQPGKLEWVSGINMGSTGYADVGRFTISRDNKNSLYLQNNSLRAEDTAVYYCA 119  
QY 120 RMRAPVLTWQGTLLVTVSRGGSGGGGSSSELTPDPAVSVALGQTVRTICQDSL 178  
DB 120 RMRAPVLTWQGTLLVTVSRGGSGGGGSSSELTPDPAVSVALGQTVRTICQDSL 179  
QY 179 RSTYASWYQKPGQAPVLTLYGKNNRPSGIPDRFGSSSGNTASLTITGAQAEADYYC 238  
DB 180 RSTYASWYQKPGQAPVLTLYGKNNRPSGIPDRFGSSSGNTASLTITGAQAEADYYC 239  
QY 239 NSRDSGNNHVPFGGGLTVLGAABEOKLISEEDLNGAA 277  
DB 240 NSRDSGNNHVPFGGGLTVLGAABEOKLISEEDLNGAA 278

## RESULT 5

US-09-079-029-11

Sequence 11, Application US/09079029

Patent No. 6342369

GENERAL INFORMATION:

APPLICANT: Adams, Camilla W.

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Chuntharapai, Anan

TITLE OF INVENTION: Apo-2 Receptor

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPacIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/079, 029

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1101R2

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 310 amino acids

TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-11

Query Match 67.6%; Score 973; DB 3; Length 310;  
Best Local Similarity 71.9%; Pred. No. 8.9e-71;  
Matches 200; Conservative 19; Mismatches 43; Indels 16; Gaps 4;

QY 16 AAOPMABEVQVSGGGGVRPGGSLRLSCAAGFTPDYDYGMSWVROAPGKLEWVSGIN 75  
DB 33 AAOPMABEVQVSGGGGVRPGGSLRLSCAAGFTPDYDYGMSWVROAPGKLEWVSGIN 92  
QY 76 NGSGTGYADVGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARMRAPV---IWQGT 132  
DB 93 DGNKTYADVGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARMRAPV---IWQGT 152  
QY 133 VTVSRGGSGGGGSGGGGSSSELTPDPAVSVALGQTVRTICQDSL---STYASWYQ 188  
DB 153 VTVSRGGSGGGGSGGGGSSSELTPDPAVSVALGQTVRTICQDSL---STYASWYQ 212  
QY 189 KPGQAPVLTLYGKNNRPSGIPDRFGSSSGNTASLTITGAQAEADYYCNSRDSGNNH 248  
DB 213 LPTAPKLLTYDSDNRPSPGIPDRFGSSSGNTASLTITGAQAEADYYCNSRDSGNNH 272  
QY 249 VFGGGLTVLGA-----AAEOKLISEEDLNGAA 277  
DB 273 VFGGGLTVLGA-----AAEOKLISEEDLNGAA 310

## RESULT 6

US-08-564-164A-2

Sequence 2, Application US/08564164A

Patent No. 615947

GENERAL INFORMATION:

APPLICANT: Schweighofer, Fabien

APPLICANT: Tocque, Bruno

TITLE OF INVENTION: Intracellular Binding Proteins and Use

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Road, 3C43

CITY: Collegeville

STATE: PA

COUNTRY: USA

ZIP: 19426-0107

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/564,164A

FILING DATE: 28-DEC-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/FR94/00714

FILING DATE: 15-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 93/07241

FILING DATE: 16-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Savitzky, Martin F.

REGISTRATION NUMBER: 29,699

REFERENCE/DOCKET NUMBER: ST93030-US

TELEPHONE: (610)454-3816

TELEFAX: (610)454-3808

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 284 amino acids

TYPE: amino acid

TOPOLOGY: linear





```
Sequence 2, Application US/09192854
Patent No. 6696245
GENERAL INFORMATION:
APPLICANT: Winter, Greg
TITLE OF INVENTION: Methode for Selecting Functional Peptides
FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
EARLIER FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-192-854-2
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Query Match          55.8%; Score 803; DB 4; Length 240;
Best Local Similarity 66.2%; Pred. No. 3,3e-57;
Matches 153; Conservative 27; Mismatches 48; Indels 6; Gaps 4;
```

```
QY 23 EVQLVESGGGVVRRPGSGLRLSCAASGFTPDYGMNWVROAPGKGLEWVSGINMGSGTGY 82
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 EVQLVESGGGVVRRPGSGLRLSCAASGFTPDYGMNWVROAPGKGLEWVSGINMGSGTGY 60
DB 83 ADSVKGFITISRDNAKSLYLOMNSLRADETAVYYCARMAPV-ITWGQGLTVYSSRGCG 141
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 ADSVKGFITISRDNAKSLYLOMNSLRADETAVYYCARMAPV-ITWGQGLTVYSSRGCG 120
QY 142 SGGGSGSGGSS--ELTQDP-AVSVALGQTVRITCOGDSLSRYASWYQKPGQAPVLI 198
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
121 SGGGSGSGGSSITDIQTQSPSSLSASVGDRTYITCRASGISSTLYLWYQKPGAPVLI 180
DB 199 YGKRRPESGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNVFFGGTKLTV 258
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
181 YASASLQSGVPSRRSSGSGGTDFLTITSLQPEDFAFYTCQGSYSTNN--TFGQGTIVEI 238
QY 199 YGKRRPESGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNVFFGGTKLTV 258
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
181 YASASLQSGVPSRRSSGSGGTDFLTITSLQPEDFAFYTCQGSYSTNN--TFGQGTIVEI 238
DB 181 YASASLQSGVPSRRSSGSGGTDFLTITSLQPEDFAFYTCQGSYSTNN--TFGQGTIVEI 238

RESULT 10
US-09-184-658-63
Sequence 63, Application US/09184658
Patent No. 6030792
GENERAL INFORMATION:
APPLICANT: Olteneasa, Ivan G.
APPLICANT: Mezes, Peter S.
APPLICANT: Downes, James T.
APPLICANT: Johnson, Kimberly S.
TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
FILE REFERENCE: PC9946-A
CURRENT APPLICATION NUMBER: US/09/184,658
EARLIER FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/065,423
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 63
LENGTH: 289
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL
OTHER INFORMATION: scfv.
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)..(22)
OTHER INFORMATION: PCANTAB6 signal peptide; Val at position 1 is most
FEATURE:
OTHER INFORMATION: likely initiator Met.
NAME/KEY: DOMAIN
LOCATION: (23)..(136)
```

```
OTHER INFORMATION: 5109 VH domain.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (139)..(154)
OTHER INFORMATION: 16 amino acid linker.
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (155)..(266)
OTHER INFORMATION: 5109 VL domain.
FEATURE:
NAME/KEY: SITE
LOCATION: (270)..(279)
OTHER INFORMATION: myc tag.
FEATURE:
NAME/KEY: SITE
LOCATION: (284)..(289)
OTHER INFORMATION: His tag.
US-09-184-658-63
```

```
Query Match          55.6%; Score 800; DB 3; Length 289;
Best Local Similarity 60.3%; Pred. No. 7,2e-57;
Matches 175; Conservative 28; Mismatches 67; Indels 20; Gaps 8;
```

```
QY 1 MKYLPTAAGLLLAQAQMAEVQVLESQGVVRRPGSGLRLSCAASGFTPDYGMWVR 60
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 MKYLPTAAGLLLAQAQMAEVQVLESQGVVRRPGSGLRLSCAASGFTPDYGMWVR 60
DB 61 QAPGKLEWVSGINMGSGTGYADSVKGRFTISRDNAKSLYLOMNSLRADETAVYYCAR 120
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 QTPDKRLEWVAITINSNGLTFFYADSVKGRFTISRDNAKSLYLOMNSLRADETAVYYCAR 120
QY 121 MRAPVI-WGQGLTVYSSRGSGSGSGSGSGSGSE--LTQDP-AVSVALGQTVRITCO-- 174
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
121 GYSVYARMGQALVTVSSGGSGSGSGSGSGSGSDVYMTQPLTISVTITQGSASISCKSS 180
DB 175 -----GDSLSRYASWYQKPGQAPVLIYGNRRPESGIPDRFGSSSGNTASLTITGAQ 229
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
181 QSLGSDGLT--YLWILQRPQSPKRLIPLVSELDGCVDRFTGSGSGTDFLTIKISRAE 238
QY 230 AEDBADYYCNSRDSGNNV--VFGGTKLTVLGAABAQKLSIEDLNGAA 277
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
239 AEDLGVVYC-----CQGTFFPFTFGAGTKLE-LKAAAEQKLSIEDLNGAAA 283
DB 239 AEDLGVVYC-----CQGTFFPFTFGAGTKLE-LKAAAEQKLSIEDLNGAAA 283

RESULT 11
US-09-504-262D-63
Sequence 63, Application US/09504262D
Patent No. 6642007
GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
APPLICANT: Saltarelli, Mary J.
APPLICANT: Johnson, Kimberly S.
TITLE OF INVENTION: Assays for Measurement of Type II Collagen Fragments in Urine
FILE REFERENCE: PC101896GR - CIP of PC9946A
CURRENT APPLICATION NUMBER: US/09/504,262D
EARLIER FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.1
SEQ ID NO 63
LENGTH: 289
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 5109 scFv from clone p5109C scFv7
OTHER INFORMATION:
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL scFv.
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)..(22)
OTHER INFORMATION: PCANTAB6 signal peptide; Val at position 1 is most likely initia
OTHER INFORMATION: or Met.
```



US-09-646-028-51  
; Sequence 51, Application US/09646028  
; Patent No. 6562347  
; GENERAL INFORMATION:  
; APPLICANT: Kwak, Larry  
; APPLICANT: Blazyn, Arya  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
; FILE REFERENCE: 14014.0316/P  
; CURRENT APPLICATION NUMBER: US/09/646.028  
; CURRENT FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: 60/077.745  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 51  
; LENGTH: 348  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-51

Query Match 55.0%; Score 791.5; DB 4; Length 348;  
Best Local Similarity 64.1%; Pred. No. 4,4e-56;  
Matches 159; Conservative 26; Mismatches 52; Indels 11; Gaps 4;

QY 23 EVOLVSGGVVPPGSLRLSCAASGFTPDYKMSVWRQAPGKLEWVSGINMGSTGY 82  
DB 94 EVOLVSGGVVPPGSLRLSCAASGFTPDYKMSVWRQAPGKLEWVSGINMGSTGY 153  
QY 83 ADSVKGRFTISRDNKNSLYIQNNLSRAEDTAVYYCARMRAPV----WGQGLTVTVY-SR 137  
DB 154 ADSVKGRFTISRDNKNSLYIQNNLSRAEDTAVYYCARMRAPV----WGQGLTVTVY-SR 213  
QY 138 GGGSGGGSGGGSGGGSG--SELTQDPNAVVALGQTVRITTCQDLSR--SYTASWYQOKPG 191  
DB 214 GGGSGGGSGGGSGGGSGSVLTQPPSVSAAPGQRVTISCTGSRNSITGAGYDVMMYQKPE 273  
QY 192 QAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFG 251  
DB 274 TAPKVLIVSNNRPSGIPDRFSGSKGTSASLAITGLQLEDEGTYVQCNDLSLGLWFG 333  
QY 252 GGTKLTVL 259  
DB 334 GGTKLTVL 341

RESULT 15  
US-08-918-148-75  
; Sequence 75, Application US/08918148A  
; Patent No. 6342220  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia  
; APPLICANT: W.  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Rendly, Brian M.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Agonist Antibodies  
; FILE REFERENCE: P0979  
; CURRENT APPLICATION NUMBER: US/08/918.148A  
; CURRENT FILING DATE: 1997-08-25  
; NUMBER OF SEQ ID NOS: 79  
; SEQ ID NO 75  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: artificial  
US-08-918-148-75

Query Match 54.7%; Score 787.5; DB 3; Length 245;  
Best Local Similarity 65.2%; Pred. No. 6e-56;  
Matches 161; Conservative 28; Mismatches 51; Indels 7; Gaps 4;

QY 21 MAEVOLVESGGGVVPPGSLRLSCAASGFTPDYKMSVWRQAPGKLEWVSGINMGST 80  
DB 1 MAEVOLVGGGGVPPGSLRLSCAASGFTPDYKMSVWRQAPGKLEWVSGINMGST 60  
QY 81 GYADSVKGRFTISRDNKNSLYIQNNLSRAEDTAVYYCARMR--APVWGGTLTVTVY 137  
DB 61 YVADSVKGRFTISRDNKNSLYIQNNLSRAEDTAVYYCARWGEDAFDIWGQGLTVTVSS 120  
QY 138 GGGSGGGSGGGSGGGSG--SELTQDPNAVVALGQTVRITTCQDLSRYYASWYQOKPGQAPV 195  
DB 121 GGGSGGGSGGGSGGGSDIVMTQSPVLSASVGRVAILTCASGCIYHMLAMTQKPGAPK 180  
QY 196 LVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVVFGGCTK 255  
DB 181 LLIYKASLSLAGAPSRFSGSGGADFTLITSLQPPDPATYYC--QQYSNYPILTFGGGCTK 238  
QY 256 LTVLGAA 262  
DB 239 LEYKRAA 245

Search completed: April 25, 2005, 21:12:13  
Job time : 44.6863 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 20:22:46 ; Search time 122.531 Seconds  
(without alignments)  
752.325 Million cell updates/sec

Title: US-10-029-926D-25

Perfect score: 1440  
Sequence: 1 MKTLPTAAAGLLLAQPA.....VLGAABQKISEEDINGAA 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubppa/PTCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubppa/PTCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubppa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubppa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubppa/US09C\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubppa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubppa/US10C\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubppa/US10C\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1440	100.0	277	US-10-032-037B-25	Sequence 25, Appl
2	1440	100.0	277	US-10-029-988B-25	Sequence 25, Appl
3	1440	100.0	277	US-10-032-423A-25	Sequence 25, Appl
4	1440	100.0	277	US-10-029-926B-25	Sequence 25, Appl
5	1416	98.3	277	US-10-032-037B-203	Sequence 203, Appl
6	1416	98.3	277	US-10-029-988B-203	Sequence 203, Appl
7	1416	98.3	277	US-10-032-423A-203	Sequence 203, Appl
8	1416	98.3	277	US-10-029-926B-203	Sequence 203, Appl
9	1388.5	96.4	280	US-10-880-922-6	Sequence 6, Appl
10	1379.5	95.8	280	US-10-880-922-5	Sequence 5, Appl
11	1379.5	95.8	280	US-10-880-922-56	Sequence 56, Appl
12	1378.5	95.7	280	US-10-880-922-60	Sequence 60, Appl
13	1378	95.7	266	US-10-032-037B-204	Sequence 204, Appl

14	1378	95.7	266	US-10-029-988B-204	Sequence 204, Appl
15	1378	95.7	266	US-10-032-423A-204	Sequence 204, Appl
16	1375.5	95.5	280	US-10-880-922-61	Sequence 61, Appl
17	1374.5	95.5	280	US-10-880-922-55	Sequence 55, Appl
18	1294	89.9	291	US-10-406-830-6	Sequence 6, Appl
19	1275.5	88.6	309	US-10-052-798-9	Sequence 9, Appl
20	1275.5	88.6	309	US-10-288-917-9	Sequence 9, Appl
21	1275.5	88.6	309	US-10-423-448-9	Sequence 9, Appl
22	1218.5	84.6	239	US-09-880-748-937	Sequence 937, Appl
23	1218.5	84.6	239	US-09-880-748-2038	Sequence 2038, Appl
24	1212.5	84.2	239	US-09-880-748-2038	Sequence 2038, Appl
25	1212.5	84.2	239	US-10-293-418-2038	Sequence 2, Appl
26	1201.5	83.4	290	US-09-969-748C-2	Sequence 2, Appl
27	1201.5	83.4	290	US-09-949-039-2	Sequence 10, Appl
28	1194	82.9	312	US-10-052-798-10	Sequence 10, Appl
29	1194	82.9	312	US-10-288-917-10	Sequence 10, Appl
30	1194	82.9	312	US-10-423-448-10	Sequence 10, Appl
31	1191.5	82.7	239	US-09-880-748-2015	Sequence 2015, Appl
32	1191.5	82.7	239	US-10-293-418-2015	Sequence 2015, Appl
33	1188.5	82.5	296	US-09-969-748C-12	Sequence 12, Appl
34	1188.5	82.5	296	US-09-949-039-75	Sequence 75, Appl
35	1178	81.8	244	US-10-322-673-42	Sequence 42, Appl
36	1139.5	79.1	239	US-09-880-748-2018	Sequence 2018, Appl
37	1139.5	79.1	239	US-10-293-418-2018	Sequence 2018, Appl
38	1133	78.7	244	US-10-322-673-45	Sequence 45, Appl
39	1132.5	78.6	239	US-09-880-748-2035	Sequence 2035, Appl
40	1132.5	78.6	239	US-10-293-418-2035	Sequence 2035, Appl
41	1131.5	78.6	245	US-10-322-673-43	Sequence 43, Appl
42	1131	78.5	252	US-09-880-748-1416	Sequence 1416, Appl
43	1131	78.5	252	US-10-293-418-1416	Sequence 1416, Appl
44	1129.5	78.4	243	US-10-935-290-69	Sequence 69, Appl
45	1127.5	78.3	243	US-09-880-748-2056	Sequence 2056, Appl

## ALIGNMENTS

RESULT 1	US-10-032-037B-25
1	Sequence 25, Application US/10032037B
2	Publication No. US20040001822A1
3	GENERAL INFORMATION:
4	APPLICANT: Bio-Technology General Corp.
5	TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
6	TITLE OR INVENTION: MOETIFES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
7	FILE REFERENCE: 10793/44
8	CURRENT APPLICATION NUMBER: US/10/032,037B
9	CURRENT FILING DATE: 2001-12-31
10	PRIOR APPLICATION NUMBER: 60/258,948
11	PRIOR FILING DATE: 2000-12-29
12	NUMBER OF SEQ ID NOS: 204
13	SOFTWARE: FastSeq for Windows Version 3.0
14	SEQ ID NO 25
15	LENGTH: 277
16	TYPE: PRT
17	ORGANISM: Homo sapiens
18	US-10-032-037B-25
19	Query Match 100.0%; Score 1440; DB 15; Length 277;
20	Best Local Similarity 100.0%; Pred. No. 6; 1e-90;
21	Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
22	Db
23	QY 1 MKTLPTAAAGLLLAQPA...VLGAABQKISEEDINGAA 277
24	1 MKTLPTAAAGLLLAQPA...VLGAABQKISEEDINGAA 277
25	QY 61 QAPGKGLVWVSGINWNGSTGVADSVKGRFTISRDAKNSLYYQNMSLRAEDPAVYYCAR 120
26	61 QAPGKGLVWVSGINWNGSTGVADSVKGRFTISRDAKNSLYYQNMSLRAEDPAVYYCAR 120
27	Db
28	QY 121 MRAPVIMGGQTLVTVSRGGGSGGGSGGGSSSLTQDPVAVYALGQTVRITCGDSLRS 180
29	121 MRAPVIMGGQTLVTVSRGGGSGGGSGGGSSSLTQDPVAVYALGQTVRITCGDSLRS 180
30	Db

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QY 181 YYASWTQOKRGAAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
DB 181 YYASWTQOKRGAAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
QY 241 RDSSGNHVVFVGSGTKLTVLGAAAEQKLISEBDLNGAA 277
DB 241 RDSSGNHVVFVGSGTKLTVLGAAAEQKLISEBDLNGAA 277

RESULT 2
US-10-029-988B-25
; Sequence 25, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-25

Query Match 100.0%; Score 1440; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 6,1e-90;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTLLPTAAAGLLILAAQAPMAEVQLVESGGGVYRRPGSGIRLSCASGFTFDYGMGSMWR 60
DB 1 MKTLLPTAAAGLLILAAQAPMAEVQLVESGGGVYRRPGSGIRLSCASGFTFDYGMGSMWR 60
QY 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADETAVYYCAR 120
DB 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADETAVYYCAR 120
QY 121 MRAPVIMGGSTLTVTRSGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQGSILRS 180
DB 121 MRAPVIMGGSTLTVTRSGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQGSILRS 180
QY 181 YYASWTQOKRGAAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
DB 181 YYASWTQOKRGAAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
QY 241 RDSSGNHVVFVGSGTKLTVLGAAAEQKLISEBDLNGAA 277
DB 241 RDSSGNHVVFVGSGTKLTVLGAAAEQKLISEBDLNGAA 277

RESULT 3
US-10-032-423A-25
; Sequence 25, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-25

Query Match 100.0%; Score 1440; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 6,1e-90;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTLLPTAAAGLLILAAQAPMAEVQLVESGGGVYRRPGSGIRLSCASGFTFDYGMGSMWR 60
DB 1 MKTLLPTAAAGLLILAAQAPMAEVQLVESGGGVYRRPGSGIRLSCASGFTFDYGMGSMWR 60
QY 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADETAVYYCAR 120
DB 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADETAVYYCAR 120
QY 121 MRAPVIMGGSTLTVTRSGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQGSILRS 180
DB 121 MRAPVIMGGSTLTVTRSGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQGSILRS 180
QY 181 YYASWTQOKRGAAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
DB 181 YYASWTQOKRGAAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
QY 241 RDSSGNHVVFVGSGTKLTVLGAAAEQKLISEBDLNGAA 277
DB 241 RDSSGNHVVFVGSGTKLTVLGAAAEQKLISEBDLNGAA 277
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```
RESULT 4
US-10-029-926B-25
; Sequence 25, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HANGY, et al
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-25

Query Match 100.0%; Score 1440; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 6,1e-90;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTLLPTAAAGLLILAAQAPMAEVQLVESGGGVYRRPGSGIRLSCASGFTFDYGMGSMWR 60
DB 1 MKTLLPTAAAGLLILAAQAPMAEVQLVESGGGVYRRPGSGIRLSCASGFTFDYGMGSMWR 60
QY 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADETAVYYCAR 120
DB 61 QAPGKLEWVSGINMNGSGTGYADSVKGRFTISRDNAKNSLYIQMNSLRADETAVYYCAR 120
QY 121 MRAPVIMGGSTLTVTRSGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQGSILRS 180
DB 121 MRAPVIMGGSTLTVTRSGGGSGGGSSSELTQDPAVSVVALGQTVRITTCQGSILRS 180
QY 181 YYASWTQOKRGAAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
DB 181 YYASWTQOKRGAAPVIVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYYCNS 240
QY 241 RDSSGNHVVFVGSGTKLTVLGAAAEQKLISEBDLNGAA 277
DB 241 RDSSGNHVVFVGSGTKLTVLGAAAEQKLISEBDLNGAA 277
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FILE REFERENCE: 10793/50  
CURRENT APPLICATION NUMBER: US/10/029,926B  
CURRENT FILING DATE: 2001-12-31  
PRIOR APPLICATION NUMBER: 60/258,948  
PRIOR FILING DATE: 12/29/2000  
NUMBER OF SEQ ID NOS: 203  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 203  
LENGTH: 277  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-029-926B-203

Query Match 98.3%; Score 1416; DB 15; Length 277;  
Best Local Similarity 98.2%; Pred. No. 2,6e-88;  
Matches 272; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKYLLPTAAAGLLLLAOPMAAEVOLVESGGGVRRPGSLRLSCAASGFTFDDYGMKSWR 60  
1 MKYLLPTAAAGLLLLAOPMAAEVOLVESGGGVRRPGSLRLSCAASGFTFDDYGMKSWR 60  
DB 61 QAGKGLIEWVSGINMGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVYYCAR 120  
61 QAGKGLIEWVSGINMGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVYYCAR 120  
QY 121 MRAPVIMWGQGLTVTSRGGGSGGGSSSELTQDPAVSVALGQTVRITCGDS 180  
121 LTPHYRMGQGLTVTSRGGGSGGGSSSELTQDPAVSVALGQTVRITCGDS 180  
DB 181 YVASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240  
181 YVASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNS 240  
QY 241 RDSGSGNHVVFSGGKTLTVLGAABQKLISEEDLNGAA 277  
181 RDSGSGNHVVFSGGKTLTVLGAABQKLISEEDLNGAA 277  
DB 241 RDSGSGNHVVFSGGKTLTVLGAABQKLISEEDLNGAA 277

RESULT 9  
US-10-880-922-6  
Sequence 6, Application US/10880922  
Publication No. US20050069955A1

GENERAL INFORMATION:  
APPLICANT: PLAKSIN, DANIEL  
APPLICANT: LEVANON, AVIGDOR  
APPLICANT: SZANTON, ESTHER  
APPLICANT: HAGAY, YOCHAVED  
APPLICANT: BEN-LEVY, RACHEL  
APPLICANT: NISGAV, Yael  
APPLICANT: KANFI, YARIV  
TITLE OF INVENTION: ANTIBODIES AND USES THEREOF  
FILE REFERENCE: 10793-143  
CURRENT APPLICATION NUMBER: US/10/880,922  
CURRENT FILING DATE: 2004-06-30  
PRIOR APPLICATION NUMBER: 60/484,061  
PRIOR FILING DATE: 2003-06-30  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 6  
LENGTH: 280  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: consensus antibody  
US-10-880-922-6

Query Match 96.4%; Score 1388.5; DB 17; Length 280;  
Best Local Similarity 96.8%; Pred. No. 1.9e-86;  
Matches 271; Conservative 0; Mismatches 6; Indels 3; Gaps 1;  
QY 1 MKYLLPTAAAGLLLLAOPMAAEVOLVESGGGVRRPGSLRLSCAASGFTFDDYGMKSWR 57  
1 MKYLLPTAAAGLLLLAOPMAAEVOLVESGGGVRRPGSLRLSCAASGFTFDDYGMKSWR 57

DB 1 MKYLLPTAAAGLLLLAOPMAAEVOLVESGGGVRRPGSLRLSCAASGFTFDDYGMKSWR 60  
1 MKYLLPTAAAGLLLLAOPMAAEVOLVESGGGVRRPGSLRLSCAASGFTFDDYGMKSWR 60  
QY 58 WYRQAPKGLIEWVSGINMGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVYY 117  
58 WYRQAPKGLIEWVSGINMGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVYY 117  
DB 61 WYRQAPKGLIEWVSGINMGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVYY 120  
61 WYRQAPKGLIEWVSGINMGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVYY 120  
QY 118 CARMRAPVIMWGQGLTVTSRGGGSGGGSSSELTQDPAVSVALGQTVRITCGDS 177  
118 CARMRAPVIMWGQGLTVTSRGGGSGGGSSSELTQDPAVSVALGQTVRITCGDS 177  
DB 121 CARMRAPVIMWGQGLTVTSRGGGSGGGSSSELTQDPAVSVALGQTVRITCGDS 180  
121 CARMRAPVIMWGQGLTVTSRGGGSGGGSSSELTQDPAVSVALGQTVRITCGDS 180  
QY 178 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 237  
178 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 237  
DB 181 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 240  
181 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 240  
QY 238 CNSRDSGSGNHVVFSGGKTLTVLGAABQKLISEEDLNGAA 277  
238 CNSRDSGSGNHVVFSGGKTLTVLGAABQKLISEEDLNGAA 277  
DB 241 CNSRDSGSGNHVVFSGGKTLTVLGAABQKLISEEDLNGAA 280  
241 CNSRDSGSGNHVVFSGGKTLTVLGAABQKLISEEDLNGAA 280

RESULT 10  
US-10-880-922-5

Sequence 5, Application US/10880922  
Publication No. US20050069955A1  
GENERAL INFORMATION:  
APPLICANT: PLAKSIN, DANIEL  
APPLICANT: LEVANON, AVIGDOR  
APPLICANT: SZANTON, ESTHER  
APPLICANT: HAGAY, YOCHAVED  
APPLICANT: BEN-LEVY, RACHEL  
APPLICANT: NISGAV, Yael  
APPLICANT: KANFI, YARIV  
TITLE OF INVENTION: ANTIBODIES AND USES THEREOF  
FILE REFERENCE: 10793-143  
CURRENT APPLICATION NUMBER: US/10/880,922  
CURRENT FILING DATE: 2004-06-30  
PRIOR APPLICATION NUMBER: 60/484,061  
PRIOR FILING DATE: 2003-06-30  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 5  
LENGTH: 280  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: consensus antibody  
US-10-880-922-5

Query Match 95.8%; Score 1379.5; DB 17; Length 280;  
Best Local Similarity 96.1%; Pred. No. 7.7e-86;  
Matches 269; Conservative 1; Mismatches 7; Indels 3; Gaps 1;

QY 1 MKYLLPTAAAGLLLLAOPMAAEVOLVESGGGVRRPGSLRLSCAASGFTFDDYGMKSWR 57  
1 MKYLLPTAAAGLLLLAOPMAAEVOLVESGGGVRRPGSLRLSCAASGFTFDDYGMKSWR 57  
DB 1 MKYLLPTAAAGLLLLAOPMAAEVOLVESGGGVRRPGSLRLSCAASGFTFDDYGMKSWR 60  
1 MKYLLPTAAAGLLLLAOPMAAEVOLVESGGGVRRPGSLRLSCAASGFTFDDYGMKSWR 60  
QY 58 WYRQAPKGLIEWVSGINMGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVYY 117  
58 WYRQAPKGLIEWVSGINMGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVYY 117  
DB 61 WYRQAPKGLIEWVSGINMGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVYY 120  
61 WYRQAPKGLIEWVSGINMGSGTGYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVYY 120  
QY 118 CARMRAPVIMWGQGLTVTSRGGGSGGGSSSELTQDPAVSVALGQTVRITCGDS 177  
118 CARMRAPVIMWGQGLTVTSRGGGSGGGSSSELTQDPAVSVALGQTVRITCGDS 177  
DB 121 CARMRAPVIMWGQGLTVTSRGGGSGGGSSSELTQDPAVSVALGQTVRITCGDS 180  
121 CARMRAPVIMWGQGLTVTSRGGGSGGGSSSELTQDPAVSVALGQTVRITCGDS 180  
QY 178 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 237  
178 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 237  
DB 181 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 240  
181 LRSYASWYQQRKGOAPVLVYIGKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYY 240  
QY 238 CNSRDSGSGNHVVFSGGKTLTVLGAABQKLISEEDLNGAA 277  
238 CNSRDSGSGNHVVFSGGKTLTVLGAABQKLISEEDLNGAA 277  
DB 241 CNSRDSGSGNHVVFSGGKTLTVLGAABQKLISEEDLNGAA 280  
241 CNSRDSGSGNHVVFSGGKTLTVLGAABQKLISEEDLNGAA 280





Db 181 YYASWYQKPGQAPVLYVYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240  
 QY 241 RDSSGNHVVFGGCTKLTVLGAAAEOK 266  
 Db 241 RDSSGNHVVFGGCTKLTVLGAAAKAK 266

## RESULT 14

US-10-029-988B-204  
 ; Sequence 204, Application US/10029988B  
 ; Publication No. US20040001839A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bio-Technology General Corp.  
 ; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
 ; FILE REFERENCE: 10793/46  
 ; CURRENT APPLICATION NUMBER: US/10/029,988B  
 ; CURRENT FILING DATE: 2001-12-31  
 ; PRIOR APPLICATION NUMBER: 60/258,948  
 ; PRIOR FILING DATE: 2000-12-29  
 ; NUMBER OF SEQ ID NOS: 204  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 204  
 ; LENGTH: 266  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-029-988B-204

Query Match 95.7%; Score 1378; DB 15; Length 266;  
 Best Local Similarity 99.2%; Pred. No. 9.3e-86;  
 Matches 264; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKYLPTAAAGLLLLAOPMAAEVOLVESGGGVPRPGSLRLSCAASGFTPDYGMWVR 60  
 Db 1 MKYLPTAAAGLLLLAOPMAAEVOLVESGGGVPRPGSLRLSCAASGFTPDYGMWVR 60  
 QY 61 QAPGKLEWVSGINMNGSGTYADSVKGRFTISRDNKNSLYIQMNSLRRAEDTAIVYYCAR 120  
 Db 61 QAPGKLEWVSGINMNGSGTYADSVKGRFTISRDNKNSLYIQMNSLRRAEDTAIVYYCAR 120  
 QY 121 MRAPVIMGGCTLVTVSRGGSGSGGSSSELTQDPAVSVALGQTVRITCQGDLSRS 180  
 Db 121 MRAPVIMGGCTLVTVSRGGSGSGGSSSELTQDPAVSVALGQTVRITCQGDLSRS 180  
 QY 181 YYASWYQKPGQAPVLYVYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240  
 Db 181 YYASWYQKPGQAPVLYVYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240  
 QY 241 RDSSGNHVVFGGCTKLTVLGAAAEOK 266  
 Db 241 RDSSGNHVVFGGCTKLTVLGAAAKAK 266

## RESULT 15

US-10-032-423A-204  
 ; Sequence 204, Application US/10032423A  
 ; Publication No. US20040002450A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bio-Technology General Corp.  
 ; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
 ; FILE REFERENCE: 10793/45  
 ; CURRENT APPLICATION NUMBER: US/10/032,423A  
 ; CURRENT FILING DATE: 2001-12-31  
 ; PRIOR APPLICATION NUMBER: 60/258,948  
 ; PRIOR FILING DATE: 12/29/2000  
 ; NUMBER OF SEQ ID NOS: 204  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 204  
 ; LENGTH: 266  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

## US-10-032-423A-204

Query Match 95.7%; Score 1378; DB 15; Length 266;  
 Best Local Similarity 99.2%; Pred. No. 9.3e-86;  
 Matches 264; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKYLPTAAAGLLLLAOPMAAEVOLVESGGGVPRPGSLRLSCAASGFTPDYGMWVR 60  
 Db 1 MKYLPTAAAGLLLLAOPMAAEVOLVESGGGVPRPGSLRLSCAASGFTPDYGMWVR 60  
 QY 61 QAPGKLEWVSGINMNGSGTYADSVKGRFTISRDNKNSLYIQMNSLRRAEDTAIVYYCAR 120  
 Db 61 QAPGKLEWVSGINMNGSGTYADSVKGRFTISRDNKNSLYIQMNSLRRAEDTAIVYYCAR 120  
 QY 121 MRAPVIMGGCTLVTVSRGGSGSGGSSSELTQDPAVSVALGQTVRITCQGDLSRS 180  
 Db 121 MRAPVIMGGCTLVTVSRGGSGSGGSSSELTQDPAVSVALGQTVRITCQGDLSRS 180  
 QY 181 YYASWYQKPGQAPVLYVYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240  
 Db 181 YYASWYQKPGQAPVLYVYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNS 240  
 QY 241 RDSSGNHVVFGGCTKLTVLGAAAEOK 266  
 Db 241 RDSSGNHVVFGGCTKLTVLGAAAKAK 266

Search completed: April 25, 2005, 21:09:47  
 Job time : 122.531 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: April 25, 2005, 19:57:16 ; Search time 31.9379 Seconds

(without alignments)  
834.495 Million cell updates/sec

Title: US-10-029-926d-25

Perfect score: 1440

Sequence: 1 MKYLPTAAAGLLILAAQPA.....VLGAAGQKLISEEDLNGAA 277

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	643.5	44.7	268	2 A56446	Ig heavy chain V r
2	568	39.4	109	2 S19663	Ig lambda chain V
3	565.5	39.3	249	2 S41374	single chain Fv an
4	562	39.0	108	2 S47184	Ig lambda chain -
5	551.5	38.3	110	2 S36272	Ig lambda chain V
6	546	37.9	127	2 S70444	Ig lambda chain pr
7	541	37.6	108	2 S38498	Ig lambda chain -
8	539	37.4	109	2 S38496	Ig lambda chain -
9	530.5	36.8	233	2 S25748	Ig lambda chain -
10	527	36.6	108	1 L3HUSH	Ig lambda chain V-
11	522.5	36.3	233	2 JCS322	p53 specific singl
12	518.5	36.0	110	2 S19672	Ig lambda chain V-
13	518	36.0	146	2 S02083	Ig lambda chain V-
14	513	35.6	98	2 S26928	Ig heavy chain V r
15	510.5	35.5	128	2 S31595	Ig heavy chain V r
16	503	34.9	96	2 S36060	Ig lambda chain -
17	503	34.9	115	2 S13726	Ig lambda chain -
18	503	34.9	121	2 S31118	Ig heavy chain - h
19	502.5	34.9	233	2 S25741	Ig lambda chain -
20	502	34.9	123	2 S30532	Ig heavy chain V r
21	501	34.8	121	2 S31104	Ig heavy chain (su
22	495.5	34.4	112	2 PH1654	Ig heavy chain V r
23	491	34.1	120	2 S36273	Ig heavy chain V r
24	489.5	34.0	145	2 S11239	Ig heavy chain V r
25	489	33.9	134	2 S31699	Ig heavy chain V r
26	488	33.8	138	2 S31666	Ig heavy chain V r
27	486	33.7	160	2 S05271	Ig heavy chain pre
28	485.5	33.7	120	2 S44111	Ig heavy chain V-D
29	485	33.7	119	2 S31108	Ig heavy chain - h

30	484.5	33.6	120	2 S48798	Ig heavy chain V r
31	482	33.5	119	2 S31107	Ig heavy chain - h
32	480	33.3	121	2 I55673	Ig heavy chain - h
33	480	33.3	123	2 S31114	Ig heavy chain - h
34	478	33.2	119	2 D36005	Ig heavy chain V r
35	478	33.2	140	2 S31686	Ig heavy chain V r
36	477	33.1	139	2 I37781	Ig variable region
37	476	33.1	119	2 C36005	Ig heavy chain V r
38	474.5	33.0	140	2 S70442	Ig heavy chain pre
39	474.5	33.0	147	2 I37780	Ig variable region
40	474.5	33.0	151	2 A60943	Ig heavy chain pre
41	474	32.9	135	2 S31598	Ig heavy chain V r
42	473.5	32.9	124	2 S20782	Ig heavy chain V r
43	473.5	32.9	128	2 S26790	Ig heavy chain V r
44	473	32.8	127	2 S38489	Ig heavy chain - h
45	472	32.8	98	2 S26927	Ig heavy chain V r

#### ALIGNMENTS

##### RESULT 1

A56446 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996

C/Accession: A56446

R/Ting, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident

A/Reference number: A56446; MUID:95229583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TAN>

A/Cross-references: GB:U20617

C/Keywords: heterotetramer; immunoglobulin

Query Match 44.7%; Score 643.5; DB 2; Length 268;  
Best Local Similarity 51.3%; Pred. NO. 4.4e-36;  
Matches 139; Conservative 35; Mismatches 80; Indels 17; Gaps 6;

QY	21	MAEVLVESGGGVVPRGSGRLSCAASGFTPDYGMHWQAQPGLEWYSGINMGST	80
DB	1	MAQVKLOESGAEIVKGCASVYKLSCTSGFRIKDTVMHWQKRGGLFWIGRIAPANGIT	60
QY	81	GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCAR--MRAVPIWGQGLTVTSR	137
DB	61	KYDPKFGKATIAADTSSNTAVYQLSLTSEDTAVYYCASVYLTREYVWGQGLTVTS	120
QY	138	GGGSGGGSGGGSGGSS-ELTQDPAV--SVALGQVVRITCGDSLRSTYASVYQKPGQAPV	195
DB	121	GGGSGGGSGGGSGGSDILQSPAIMSASISGEKVMSCRASSSVN-FIYVYQKSDSPK	179
QY	196	LVIYVGNKRPSPGIPDRFGSSSGNTASLTITGAQAEADYVNCNRSRDSGNHVPFGG	255
DB	180	LMVYVTSHPVPGVPAFSGSGSGNSYSLTISSEGEDAATYYCOQPTSS--PFTFGSG	237
QY	256	LTVLGA-----AABQKLISEEDLNGAA 277	
DB	238	LEIKRMAHHHHHGAAGQKLISEEDLNGAA 268	

##### RESULT 2

S19663 Ig lambda chain V region (clone alpha-B5A3) - human

C/Species: Homo sapiens (man)

C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000

C/Accession: S19663

R/Marke, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter

J. Mol. Biol. 222, 581-597, 1991

A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p

A/Accession: S19663  
 A/Molecule type: mRNA  
 A/Residues: 1-109 <MRA>  
 C/Cross-references: EMBL:X61640; NID:g29492; PIDN:CAA43821.1; PID:g1340166  
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 39.4%; Score 568; DB 2; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-31;  
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 SSELTDPAVVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNKPPSGIPDR 211  
 DB 1 SSELTDPAVVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNKPPSGIPDR 60

QY 212 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFQGGTKLTVLG 260  
 DB 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFQGGTKLTVLG 109

## RESULT 3

S41374  
 Ig lambda chain Fv antibody - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
 C/Accession: S41374  
 R/Artsemko, O.; Weller, E.W.; Muentz, K.; Conrad, U.

Submitted to the EMBL Data Library, January 1994  
 A/Description: Construction and functional characterization of a single chain Fv antibody  
 A/Reference number: S41374  
 A/Accession: S41374  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-249 <ART>  
 A/Cross-references: EMBL:Z29480

Query Match 39.3%; Score 565.5; DB 2; Length 249;  
 Best Local Similarity 48.2%; Pred. No. 6.5e-31;  
 Matches 123; Conservative 37; Mismatches 74; Indels 21; Gaps 6;

QY 23 EVOLVESGGVVPGGSLRSCAAGTTPDYGKSWYQAPKGLKLEWVSGINMGSTGY 82  
 DB 1 OVALOOSGALVVRPGASVSKLCTASGFNFDDYIHWKQBPKEGLEWIAIAPASGVKY 60

QY 83 ADVKGRFTSRNKKSKYLQNSLAEDTAYVYCAR---WRAPYKOGTLVYMSRG 138  
 DB 61 VPRFQDAVTTADTSSNTAYLLSLTSEDTAYVYCARDTLYTSLGYWQGSTVTVSSR 120

QY 139 GGGSGGGSGGGSS-ELTOD-PAVSVALGQTVRITCO-----GDSLSRYASWYQ 187  
 DB 121 GGGSGGGSGGGSDIELTOSPSVYVIPGESVISCRSSKSLYSDGS-----YLFWFL 176

QY 188 QKPGQAPVLVIYGNKPPSGIPDRFSGSSGNTASLTITGAQAEDEADYYCNSRDSGNH 247  
 DB 177 QKPGQAPVLVIYGNKPPSGIPDRFSGSSGNTASLTITGAQAEDEADYYCNSRDSGNH 247

QY 248 VVFGGTKLTVLGA 262  
 DB 235 LTFGAGTKLEKRA 249

## RESULT 4

S47184  
 Ig lambda chain - human  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C/Accession: S47184  
 R/McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.

Submitted to the EMBL Data Library, June 1994  
 A/Description: Cloning and analysis of Igm anti-thyroglobulin autoantibodies from patient  
 A/Reference number: S47181  
 A/Accession: S47184

A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-108 <MCIS>  
 C/Cross-references: EMBL:X79783; NID:g506426; PIDN:CAA56179.1; PID:g506427  
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 39.0%; Score 562; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-31;  
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 SSELTDPAVVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNKPPSGIPDR 211  
 DB 1 SSELTDPAVVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNKPPSGIPDR 60

QY 212 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFQGGTKLTVL 259  
 DB 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFQGGTKLTVL 108

## RESULT 5

S36272  
 Ig lambda chain V region (clone alpha-THY-29) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
 C/Accession: S36272  
 R/Giffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993  
 A/Title: Human anti-self antibodies with high specificity from phage display libraries.  
 A/Reference number: S36256; M0ID:93178448; PMID:7679990  
 A/Accession: S36272  
 A/Status: preliminary; nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-110 <GRI>

A/Cross-references: EMBL:Z18833; NID:g33419; PIDN:CAA79285.1; PID:g933912  
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F/15-89/Domain: immunoglobulin homology <IMM>

Query Match 38.3%; Score 551.5; DB 2; Length 110;  
 Best Local Similarity 98.2%; Pred. No. 2.4e-30;  
 Matches 108; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 152 SSELTDPAVVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNKPPSGIPDR 211  
 DB 1 SSELTDPAVVALGQTVRITTCGDSLSRYASWYQKPGQAPVLVIYGNKPPSGIPDR 60

QY 212 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFQGGTKLTVLG 260  
 DB 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFQGGTKLTVLG 110

## RESULT 6

S70444  
 Ig lambda chain precursor V region - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
 C/Accession: S70444; S70426  
 R/Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.

Mol. Immunol. 29, 1363-1373, 1992  
 A/Title: Igm kappa/lambda BBV human B cell clone: an early step of differentiation of F  
 A/Reference number: S70442; M0ID:93024508; PMID:1383695  
 A/Accession: S70444  
 A/Status: not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-127 <CUI>

A/Cross-references: UNIPROT:Q9NSD6  
 A/Experimental source: clone E29.1  
 R/Tonnelle, C.  
 Submitted to the EMBL Data Library, May 1990  
 A/Reference number: S70426  
 A/Accession: S70426

A:Molecule type: mRNA  
 A:Residues: 1-90 <TON>  
 A:Cross-references: EMBL:X53070  
 A:Experimental source: cell line E29.1, clone VL 29-1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:1-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>  
 F:14-108/Domain: immunoglobulin homology <IMM>

Query Match 37.9%; Score 546; DB 2; Length 127;  
 Best Local Similarity 97.2%; Pred. No. 6.5e-30;  
 Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 152 SSELTDPAVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLVIYGNRPSGIPDR 211  
 |||||  
 DB 20 SSELTDPAVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLVIYGNRPSGIPDR 79

QY 212 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLG 259  
 |||||  
 DB 80 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLG 127

RESULT 7  
 S38498  
 Ig lambda chain - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C:Accession: S38498  
 R:Mark: J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.  
 submitted to the EMBL Data Library, June 1993  
 A:Description: Human antibody fragments specific for human blood group antigens from a F.  
 A:Reference number: S38488  
 A:Accession: S38498  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-108 <NAR>  
 A:Cross-references: EMBL:Z23035; NID:G414043; PIDN:CAA80570.1; PID:G414044  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 37.6%; Score 541; DB 2; Length 108;  
 Best Local Similarity 97.2%; Pred. No. 1.2e-29;  
 Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 153 SSELTDPAVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLVIYGNRPSGIPDR 212  
 |||||  
 DB 1 SSELTDPAVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLVIYGNRPSGIPDR 60

QY 213 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLG 260  
 |||||  
 DB 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLG 108

RESULT 8  
 S38496  
 Ig lambda chain - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C:Accession: S38496  
 R:Mark: J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.  
 submitted to the EMBL Data Library, June 1993  
 A:Description: Human antibody fragments specific for human blood group antigens from a F.  
 A:Reference number: S38488  
 A:Accession: S38496  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-109 <NAR>  
 A:Cross-references: EMBL:Z23031; NID:G414039; PIDN:CAA80566.1; PID:G414040  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 37.4%; Score 539; DB 2; Length 109;  
 Best Local Similarity 93.6%; Pred. No. 1.6e-29;  
 Matches 102; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 152 SSELTDPAVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLVIYGNRPSGIPDR 211  
 |||||  
 DB 1 SSELTDPAVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLVIYGNRPSGIPDR 60

QY 212 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLG 260  
 |||||  
 DB 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLG 109

RESULT 9  
 S25748  
 Ig lambda chain - human  
 C:Species: Homo sapiens (man)  
 C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C:Accession: S25748  
 R:Combrato, G.; Klobeck, H.G.  
 Eur. J. Immunol. 21, 1513-1522, 1991  
 A:Title: V(Lambda) and J(Lambda) gene segments of the human immunoglobulin la  
 A:Reference number: S16439; PMID:91257162; PMID:1904362  
 A:Accession: S25748  
 A:Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-233 <COM>  
 A:Cross-references: EMBL:X57813; NID:G33725; PIDN:CAA0950.1; PID:G33726  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 36.8%; Score 530.5; DB 2; Length 233;  
 Best Local Similarity 83.5%; Pred. No. 1.3e-28;  
 Matches 106; Conservative 6; Mismatches 10; Indels 5; Gaps 2;

QY 152 SSELTDPAVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLVIYGNRPSGIPDR 211  
 |||||  
 DB 20 SSELTDPAVVALGQTVRTTCGDSLSRYASWYQKPGQAPVLVIYGNRPSGIPDR 79

QY 212 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFPGGKTLTVLG--AAAEQKLI 268  
 |||||  
 DB 80 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGDDQLFGGKTLTVLGPKAAPSVTLF 139

QY 269 --SEEDL 273  
 |||||  
 DB 140 PPSSEEL 146

RESULT 10  
 L3HUSH  
 Ig lambda chain V-III region (Sh) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004  
 C:Accession: A01980  
 R:Tilanti, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.  
 J. Biol. Chem. 245, 2171-2176, 1970  
 A:Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The complete  
 A:Reference number: A92057; PMID:70166723; PMID:4909564  
 A:Accession: A01980  
 A:Molecule type: protein  
 A:Residues: 1-108 <RTT>  
 A:Cross-references: UNIPROT:P01714  
 A:Note: the sequence of the C region is also given  
 C:Genetics:  
 A:Gene: GDB:IGLV@  
 A:Cross-references: GDB:119342; OMIM:147240  
 A:Map position: 22q11.2-22q11.2  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into L.  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin



QY 83 ADSVKGRFTISRDNAKNSLYLQWNSLRAPEDTAVYYCAR 120  
 |||||  
 Db 61 ADSVKGRFTISRDNAKNSLYLQWNSLRAPEDTALYHCAR 98  
 |||||

## RESULT 15

S31595  
 Ig heavy chain V region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S31595  
 R:Clisnier, A.W.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
 submitted to the EMBL Data Library, June 1992  
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
 A:Reference number: S31585  
 A:Accession: S31595  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-128 <CUI>  
 A:Cross-references: EMBL:Z14171; NID:G31007; PIDN:CA78540.1; PID:G31008  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:23-106/Domain: immunoglobulin homology <IMM>

Query Match 35.5%; Score 510.5; DB 2; Length 128;  
 Best Local Similarity 83.3%; Pred. No. 1.5e-27;  
 Matches 100; Conservative 6; Mismatches 7; Indels 7; Gaps 2;  
 QY 23 EVOLVESGGGVVRRPGSGLRLSCAASGFTPDYGMKSWVROAPGKGLEWVSGINMGSGTGY 82  
 |||||  
 Db 9 EVOLVESGGGLVQPGKSLRLSCAASGFTPDYAMHWVROAPGKGLEWVSGISWNSGSIgy 68  
 |||||  
 QY 83 ADSVKGRFTISRDNAKNSLYLQWNSLRAPEDTAVYYCARMAP-----VWGGGTLYTVS 136  
 |||||  
 Db 69 ADSVKGRFTISRDNAKNSLYLQWNSLRAPEDTALYHCAR-DAPGDHDAFDIWGGTMYTVS 127  
 |||||

Search completed: April 25, 2005, 20:24:08  
 Job time : 31.9379 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:10:00 ; Search time 143.106 seconds  
(without alignments)  
991.192 Million cell updates/sec

Title: US-10-029-926D-25  
Perfect score: 1440  
Sequence: 1 MKYLPTAAAGLLLAQPA.....VLGAAPKLIKSHEDINGAA 277

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	758	52.6	240	2	065ZC9
2	723.5	50.2	298	2	090YF0
3	715	49.7	255	2	06K805
4	693.5	48.3	248	2	065ZQ7
5	636	44.2	244	2	065ZC8
6	600	41.7	241	2	0921A6
7	578	40.1	243	2	07TOM2
8	552	38.3	107	2	09NSD6
9	550.5	38.2	112	2	09HCC1
10	548	38.1	487	2	065ZL2
11	530	36.8	233	2	06GMW4
12	527	36.6	108	1	LV3A HUMAN
13	516	35.8	472	2	06N089
14	511	35.5	489	2	08NSK4
15	508	35.3	573	2	08WU38
16	507.5	35.2	218	2	0925S1
17	483	33.5	121	2	09UL71
18	478	33.2	470	2	06PIJ4
19	478	33.2	478	2	06PIB1
20	477	33.1	606	2	06GMW2
21	474	32.9	464	2	06MZU6
22	474	32.9	613	2	08WUK1
23	473.5	32.9	597	2	096B89
24	471.5	32.7	473	2	06MZV7
25	470	32.6	113	2	09UL90
26	465	32.3	493	2	06GMX2
27	461.5	32.0	118	2	09UL91
28	457.5	31.8	475	2	06MZC6
29	456	31.7	466	2	06IN78
30	452.5	31.4	479	2	06MZV6
31	450	31.2	473	2	091Z05

32	448.5	31.1	465	2	06PE64	06PE64 homo sapien
33	446.5	31.0	116	1	HV3T HUMAN	P01781 homo sapien
34	446.5	31.0	494	2	06ZW64	06ZW64 homo sapien
35	445	30.9	479	2	091WP5	091WP5 mus musculu
36	444.5	30.9	122	1	HV3G HUMAN	P01768 homo sapien
37	444	30.8	116	2	09UL93	09UL93 homo sapien
38	443	30.8	117	1	HV3C HUMAN	P01764 homo sapien
39	441.5	30.7	494	2	096K68	096K68 homo sapien
40	440.5	30.6	483	2	06MXZ9	06MXZ9 homo sapien
41	440	30.6	485	2	06PDB8	06PDB8 mus musculu
42	439.5	30.5	544	2	06P395	06P395 homo sapien
43	439	30.5	480	2	06N094	06N094 homo sapien
44	436.5	30.3	118	2	09UL72	09UL72 homo sapien
45	436.5	30.3	475	2	06GMW7	06GMW7 homo sapien

## ALIGNMENTS

## RESULT 1

ID	065ZC9	PRELIMINARY;	PRT;	240 AA.
AC	065ZC9;			
DT	25-OCT-2004 (TREMBLrel. 28, Created)			
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)			
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DE	Single-chain Fv (Fragment).			
GN	Name=sCFv;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
NC	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C1q/7;			
RA	MEDLINE=97362799; PubMed=9219263;			
RA	Kontermann R.E., Wing M.G., Winter G.;			
RT	"Complement recruitment using bispecific diabodies.";			
RL	Nat. Biotechnol. 15:629-631(1997).			
DR	EMBL; Y13056; CAA73499.1; ..			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003596; IG_V.			
DR	Pfam; PF00047; IG_2.			
DR	SMART; SM00409; IG_2.			
DR	SMART; SM00406; IG_V_2.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
FT	NON TER 1			
FT	NON TER 240			
SQ	SEQUENCE 240 AA; 25569 MW; FDCPD3645F64B373 CRC64;			

Query Match 52.6%; Score 758; DB 2; Length 240;

Best local Similarity 62.9%; Pred. No. 1.7e-46;

Matches 151; Conservative 32; Mismatches 51; Indels 6; Gaps 4;

QY	23	EVQLVDSGGGVRRPGSLRSCASGFTDDYGMVRRQAPGKGLFMWSGIMNGSTGY 82
DB	1	QVQLVDSGGGLVPGGSLRLSCAASGFTSSYGMHWVRQAPGKGLWVAITISYDSNKTY 60
QY	83	ADSVKRFRTISRDNAKNSLYLQNSLRADDAVYYCARRAPIY--WGQSTLVTVRGGG 140
DB	61	ADSVKRFRTISRDNAKNSLYLQNSLRADDAVYYCARRAPIY--WGQSTLVTVRGGG 120
QY	141	GSQGGSGGGSGGS-ELTQDPA--VSVALGQTVRTTCGDSLRYSYASWYQKPGQAPLVLT 198
DB	121	GSQGGSGGGSGGSIDQMTQSPSTLSASIGDRVITTCRASGIIYRWLAWYQKPGKAPKLLI 180
QY	199	YGKNRPPSGIPRFSSSSSGNTASLTITGAQADEADYVYCNSSDSCGNVVFEGGKLTLY 258
DB	181	YKASLASAPSPFSSGSGGTPTLTISLQPDPAFYTC--QQYSNYPVTFEGGKLTLEI 238

RESULT 2

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DR EMBL; AJ746180; CAG34081.1; -.
DR HSPD; P01837; 1KCR.
DR InterPro; IPR003599; Ig_1like.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER
SQ SEQUENCE      255 AA; 27445 MW; B68BD3839SDF713B CRC64;

Query Match          49.7%; Score 715; DB 2; Length 255;
Best Local Similarity 58.8%; Pred. No. 2,1e-43;
Matches 147; Conservative 33; Mismatches 54; Indels 16; Gaps 6;

QY      EVQLVESGGGVAVRRGSGLRISCAASGFETPDYGMSTWRQAPKGLEWVSGINMGSTGY 82
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      1 QVLQIQSGGGLVKKPGKSLIKVSCAASGTFPSSYGMSWRQPDPKRILEVAITTSGGSYTY 60
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||

QY      ADSVKGRFTTISRDAKNKSLYLQNMSLSAEPTAVYYCARM-----RAPVIMGGCTLVTS 136
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      61 PDYSVKGRFTTISRDAKNKTLVLYQMSLSSEDTAMVCAHINRYRDKAFDYWGQGCTLLTVS 120
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||

QY      RGGGSGSGGGSGGGSGGS-ELTQDP-AVSVALGQTVRITCO-GDSL-----RSYASWYQQ 188
       |||||||
Db      121 SGGGSGSGGGSGGGSGGSIIYMAQSSTSVNAGERIVMSCSGSLNSRNQKYIAYQQ 180
       |||||||

QY      KPGCAPLVLIYGNKNRPDSGIPIPREPSGSSSGNTASLTITGAQAEDDEADYCNSRDSSGNHV 248
       |||::|
Db      181 KPQGSFLLIIRIGASTRESGVPDRFTFGSGSGNDFTLTITSVOAEDLAIVYQCNDHS--YPL 238
       |||::|

QY      249 VFGGCTKLIV 258
       |||::|
Db      239 TFGAGTKLEI 248
       |||::|

RESULT 4
065ZOT PRELIMINARY; PRT; 248 AA.
ID 065ZOT AC 065ZOT;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE B3(Fv)-PE40 (Fragment).
DE Name=B3(Fv)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92020904; PubMed=1924423;
RA Brinkmann U., Pal L.H., Fitzgerald D.J., Williamson M., Paetran I.;
RT "B3(Fv)-PE38DEL, a single-chain immunotoxin that causes complete
RL regression of a human carcinoma in mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR EMBL; S57590; AAB19971.2; -.
DR InterPro; IPR003599; IG; 2.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER
SQ SEQUENCE      248 AA; 26634 MW; 7A3759BA43E570950 CRC64;

Query Match          48.3%; Score 695.5; DB 2; Length 248;
Best Local Similarity 57.8%; Pred. No. 5,1e-42;
Matches 144; Conservative 32; Mismatches 56; Indels 17; Gaps 6;

QY      23 EVQLVESGGGVARRGGSIARLSCAASGTFPDYGMSTWRQAPGKLEWVSGINMGSTGY 82
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||

```

Dd		2	DVKLVESGGGLVQPGSGSLKLSGATCGTFFPSDYVMWVRQTPEKRLEWVAIYISNDSSNAY	61
Oy		83	ADSVAGRTTISDNNAKNSLYLOMNSLRBEDTVYYCARMRA---PVTWGGTLVTYSRG	138
Dd		62	SDTVAGRTTISDNNARNLTLYLOMSRLKSBDTAIVSCAGLAWGAFAWGQGTLVTSYG	121
Oy		139	GGGSGGGGGGGGGSSSEL-TDDP-AVSVALGQVTRTCGGDSL-----RSYASWQQXRG	191
Dd		122	GGGSGGGGGGGGGSVLTTQSPLSPVSLGDQASTSCSSSQIYHSNGTLYEWLQXRG	181
Oy		192	QAPVLVIYGNRRPFGSIDPRFSGSSSGNTASLTITGAODEADYVCNSRDSGNNH--VV	249
Dd		182	QSPKLTIYKVSNRFGGVDFRFGSSSGTDFTLKIRVAEDLGYYCC----FGSGHVFFT	237
Oy		250	FGGGTXTLTV 258	
Dd		238	FGSGTKLEI 246	
 RESULT 5 Q65ZC8 PRELIMINARY; PRT; 244 AA. Q65ZC8				
ID	Q65ZC8			
AC	Q65ZC8;			
DT	25-OCT-2004 (TREMBLrel. 28, Created)			
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)			
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DE	Single-chain Fv (fragment).			
GN	Name=scfv;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9736279; PubMed=9219263;			
RA	Kontermann R.E., Wing M.G., Winter G.;			
RT	"Complement recruitment using bispecific diabodies.";			
RL	Nat. Biotechnol. 15:629-631(1997).			
DR	EMBL; Y13057; CAA73500.1; -.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; IG; 2.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00406; IGV; 2.			
DR	PROSITE; PS00835; IG_LIKE; 2.			
FT	NON_TER 1			
FT	NON_TER 1			
SO	SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;			
 Query Match 44.2%; Score 636; DB 2; Length 244; Best Local Similarity 50.8%; Pred. No. 9,1e-38; Matches 124; Conservative 46; Mismatches 64; Indels 10; Gaps 4;				
Oy		23	EVOLVESSGGVVRPEGSLRLSCAASGFPPDDYGMKWVRQAPKGILEWVGINMGSTGY	82
Dd		1	QVOLQSGAEVKKPKPDSSVAVSCSKASGYFSDHYMHMVQRAPQGGILEMMGWIDPNNGDTRF	60
Oy		83	ADVSVGRRTISRDNANKSLYLQMNSLRBEDPAVYYCAR-----RAVINGQGLTVYVS	136
Dd		61	AORFGRGRTYMRTRDISIAAYMEVSRLRSDDPDAVYCAEEGTSALYGDWVGQGLTVVS	120
Oy		137	RCGGSGGGGGGGGGSSS-ELTPDDPA-VSVALGQVTRITCGDGSLSRYASYAQKPGQAP	194
Dd		121	SGGGSGGGGGGGGGSSDJQMTGPSFTLASIGDRTITICRASBGILYHLWAYQOKRGAP	180
Oy		195	VLVYIYGNRRPBGIDPRFSGSSSGNTASLTITGAODEADYVCNSRDSGNNHVVGGGT	254
Dd		181	KFLIYKASLSLAGASRFSGSGSGTDFTLTISLQPDDPFATYYC--QQSYNVLPFGGGT	238
Oy		255	KLTIV 258	
Dd		239	KLEI 242	

Query	Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
QY	23	EVQLVESGGGVGVRPQGSILRLSCAASGFTPDYGMNWYQAPGKGLIEWVSGINMGSSITGY	41.7%; Score 600; DB 2; Length 241;	51.9%; Pred. No. 3,4e-35;	67;	16;	6;
DB	1	QVQLQSGPELTKPKPEGITVTKISCKASGYTFDYGMMWYKQAPGKGLKMMGWINTVYGPPTY					
QY	83	ADSVKSGPFTISRDAKNSLYIQNMSLAEPDAVYYCAR--MRAPIVWGCTTVYTSRGG					
DB	61	ADDERGRARFLETSASTAYLQINNLKNEIDATYFCARKDLRFYDWGGSTVTVSSGG					
QY	140	GGSGGGSGSGGSGS-ELTDP-AVSVALGQTVRTTCGDSILRSYASWYQKPGQAL---					
DB	121	GGSGGGSGSGGSGSIELTQSPSSLSASLGKVTITTCASQDINKYIMYQHKPKGGRSA					
QY	195	-VLVIYGNRRPSPGIPDFSGSSGSSGNTASLTITCAQAEDEADYYCNSRDSGNHIVFGGG					
DB	181	HTLHAIYIQ---PGLPSRFSGSGGRDYSFSSISNLEPEDIAITYCLHYD--NLATFGGG					
QY	254	TKL 256					
DB	234	TKL 236					

RESULT 7

ID	OTOM2	PRELIMINARY;	PRT;	243 AA.
AC	OTOM2.			
DT	01-OCT-2003 (TREMBlrel. 25, Created)			
DT	01-OCT-2003 (TREMBlrel. 25, Last sequence update)			
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)			
DR	ScFv 6H8 protein (Fragment).			
GN	Name=ScFv 6H8;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Balb/C;  
 RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;  
 RA Peter J.C., Eftekhar P., Billfeld P., Wallukat G., Hoebeke U.;  
 RT "scf single chain antibody variable fragment as inverse agonist for  
 RL the beta-2 adrenergic receptor";  
 RL J. Biol. Chem. 278:36740-36747(2003).  
 DR EMBL: AJ574851; CAB00495.1; -;  
 DR HSSP: P01751; 1A6W.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_V.  
 DR SMART: SM00406; IGV; 2.  
 DR PROSITE: PSS0835; IG\_LIKE; 2.  
 FT NON TER 1  
 SQ SEQUENCE 243 AA; 25976 MW; BEPFE6AD2DC64F76 CRC64;

Query Match 40.1%; Score 578; DB 2; Length 243;  
 Best Local Similarity 49.4%; Pred. No. 1.3e-33;  
 Matches 118; Conservative 37; Mismatches 78; Indels 6; Gaps 4;

QY 23 EVLVESGGGVAPGGSRLRSCASGFTPDYGMVWROAPGKLEWVGGINNGSTGY 82  
 DB 1 QVGLQSGSELVPGASVKSASGFTFTTMMHWKQHGQGLEWIGNIYFGSGITNY 60  
 QY 83 ADSVKRFTISRDNANKSLYLQWNSLRABDTAVYCAR-ARAVINGQGLTVTVSRGGG 141  
 DB 61 DEFKKXGILTVTSSSTAYMHLSLASEDSAVYCARGRGLDWAGTTLTVSSGGG 120  
 QY 142 SGGGGSGGGSS-ELTQ-DPAVSVALGQTRITCGDSLRSYASWYQKPGQAPVLVY 139  
 DB 121 SGGGGSGGGSDIQMTGSSSPSVSLGDRVTITCKASEDIYNNLAWYQKPGAPRLLIS 180  
 QY 200 GKNNRPSGIDPRSGSSGNTASLTITGAQDEADYCNRSRSGNHVFGGTXKT 258  
 DB 181 GATSLGVPSRPSGSGSKDYTLSTLQTEDEVATYICQYQWSTR--TFGGTKLEI 236

## RESULT 8

ID Q9NSD6 PRELIMINARY; PRT; 107 AA.  
 AC Q9NSD6;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Homo sapiens This CDS feature is included to show the translation of  
 DE the corresponding V\_region. Presently translation qualifiers on  
 DE V\_region features are illegal. (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymphocyte;  
 RA Hohmann A.;  
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: LA3092; AAA69746.2; -;  
 DR FTR: S70444; S70444.  
 DR HSSP: P01709; 2MCG.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_V.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PSS0835; IG\_LIKE; 1.  
 FT NON TER 1  
 FT NON TER 107  
 SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 38.3%; Score 552; DB 2; Length 107;  
 Best Local Similarity 98.1%; Pred. No. 3.8e-32;  
 Matches 105; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 154 ELTQDPAVSVALGQTRITCGDSLRSYASWYQKPGQAPVLVYGNKNNRPSGIDPRFS 213

DB 1 ELTQDPAVSVALGQTRITCGDSLRSYASWYQKPGQAPVLVYGNKNNRPSGIDPRFS 60  
 QY 214 GSSSGNTASLTITGAQDEADYCNRSRSGNHVFGGTXKTVLG 260  
 DB 61 GSSSGNTASLTITGAQDEADYCNRSRSGNHVFGGTXKTVLG 107

## RESULT 9

ID Q9HCC1 PRELIMINARY; PRT; 112 AA.  
 AC Q9HCC1;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Single chain Fv (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB049915; BAB16829.1; -;  
 DR HSSP: P01783; 1IGC.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_V.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PSS0835; IG\_LIKE; 1.  
 FT NON TER 1  
 FT NON TER 112  
 SQ SEQUENCE 112 AA; 12243 MW; 24FLA5EC3B84788 CRC64;

Query Match 38.2%; Score 550.5; DB 2; Length 112;  
 Best Local Similarity 94.6%; Pred. No. 5.2e-32;  
 Matches 106; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 23 EVLVESGGGVAPGGSRLRSCASGFTPDYGMVWROAPGKLEWVGGINNGSTGY 82  
 DB 1 EVLVESGGGVAPGGSRLRSCASGFTPDYGMVWROAPGKLEWVGGINNGSTGY 60  
 QY 83 ADSVKRFTISRDNANKSLYLQWNSLRABDTAVYCAR-ARAVINGQGLTV 133  
 DB 61 ADSVKRFTISRDNANKSLYLQWNSLRABDTAVYCAR-ARAVINGQGLTV 112

## RESULT 10

ID Q65ZL2 PRELIMINARY; PRT; 487 AA.  
 AC Q65ZL2;  
 DT 25-OCT-2004 (Tremblrel. 28, Created)  
 DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
 DE Fv/M4.  
 GN Name=M4-IFN- $\gamma$ -<tau>;  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10095;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96272580; PubMed=8688499;  
 RA Qi Y., Xiang J.;  
 RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric  
 RT antibody secreted from myeloma cells";  
 RL Hum. Antibodies Hybridomas 6:161-166(1995).  
 DR EMBL: S82493; AAB37424.2; -;  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig\_c1.  
 DR InterPro: IPR003598; Ig\_c2.  
 DR InterPro: IPR003006; Ig\_MHC.



Best Local Similarity 92.6%; Pred. No. 2,4e-30;  
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 153 SELTQPAVSVALGQVTRITCOGDSLRSYVYVYQOKPGQAPLVLYGKNNRSGIPDRF 212  
DB 1 SELTQPAVSVALGQVTRITCOGDSLRLGYDAAMYQOPGAPLVLYGKNNRSGIPDRF 60  
QY 213 SGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTLTVLG 260  
DB 61 SGSSSGHTASLTITGAQAEDEADYYCNSRDSGNHVPFGGTLTVLG 108

## RESULT 13

Q6N089 PRELIMINARY; PRT; 472 AA.  
AC Q6N089;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein DKFZp686P15220.  
GN Name=DKFZp686P15220;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Wambolt R., Heidner D., Mewes H.W., Weil B., Amid C., Oeangger A.,  
RL Fobo G., Han M., Wiemann S.;  
RA Submitted (JUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BK40627; CAB45781.1; -  
DR HSSP; P01861; IAD0.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG-cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KM Hypothetical protein  
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 35.8%; Score 516; DB 2; Length 472;  
Best Local Similarity 47.3%; Pred. No. 7.1e-29;  
Matches 116; Conservative 20; Mismatches 77; Indels 32; Gaps 5;

QY 13 LLLAAPMAEVLVSGGGGVPRGSLRLSCAASGTFPDYGMVSWROAPGKLEWVG 72  
DB 10 LLLAALKVQCEVLVSGGGGVPRGSLRLSCAASGTFPDYGMVSWROAPGKLEWVG 69  
QY 73 INNGSGTGYADVSKRFTISRDNANKSLYLQNNSLRAEDTAVYYCAR-----MRAP 124  
DB 70 ISNNSGSIAYADVSKRFTISRDNANKSLYLQNNSLRAEDTAVYYCAKEIGAHNFYYGM 129  
QY 125 VIVGGTLVTVSRGGGGSGGGGSSSELTDPAVSVALGQTVTRITCOGDSLRSYVY 184  
DB 130 DVWGQGTITVTVS-----SASTKGPVFPPLAPFSKSTSGTAAALGC---LVKQYFPE 177  
QY 185 WYQOKPGQAPLVLYGKNNRSGI---PDRFSGSSSNTASLTITGAQAEDEADYYCNSR 241  
DB 178 -----PVTYSWNSGALTSVHTFPVALQSGLSGLVSSVTVTPSSSLGTOITICNVN 228  
QY 242 DSSGN 246  
DB 229 HKPSN 233

## RESULT 14

Q8N5K4 PRELIMINARY; PRT; 499 AA.  
AC Q8N5K4;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE MGCC27165 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mallary S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,  
RT Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

QY 13 LLLAAPMAEVLVSGGGGVPRGSLRLSCAASGTFPDYGMVSWROAPGKLEWVG 72  
DB 10 LLLAALKVQCEVLVSGGGGVPRGSLRLSCAASGTFPDYGMVSWROAPGKLEWVS 69  
QY 73 INNGSGTGYADVSKRFTISRDNANKSLYLQNNSLRAEDTAVYYCARMRAPV----- 125  
DB 70 INNGSGTGYADVSKRFTISRDNANKSLYLQNNSLRAEDTAVYYCARPTKXCSGSSCL 129  
QY 126 -----IWGGTLVTVSRGGGGSGGGGSSSELTDPAVSVALGQTVTRITCOGDSL 173  
DB 130 GYMDVWGKGTITVTVS-----SASPTSPKVPFLSLCSTQPDGNNVIACTV 174  
QY 174 QGDSLRSYVYQOKPGQAPLVLYGKNNRSGIPDRFSGSSSNTASLTIT 225  
DB 175 QG-----FPQEPPLVTVWSESGQG---VTARNFPPS---QDASGLVYTTSSQTL 218

Query Match 35.5%; Score 511; DB 2; Length 499;  
Best Local Similarity 49.6%; Pred. No. 1.7e-28;  
Matches 121; Conservative 16; Mismatches 49; Indels 58; Gaps 8;

QY 226 TGAQ 229  
Db 219 PATQ 222

RESULT 15

Q8WU38 PRELIMINARY; PRT; 573 AA.  
AC Q8WU38;  
DT 01-MAR-2002 (TREMBlrel. 20, Created)  
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Hypoetical protein.  
OS Homo sapiens (Human).  
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,  
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywnski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]

RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC021276; AAH21276.1; -  
DR PIR; S21205; S21205.  
DR PIR; S30532; S30532.  
DR HSSP; P18529; 118K.  
DR Pfam; PF07654; C1-sect; 2.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Ig; 1.  
DR PROSITE; PSS0835; IG LIKE; 4.  
DR PROSITE; PSS0290; IG\_MHC; UNKNOWN\_2.  
KM Hypoetical protein.  
SQ SEQUENCE 573 AA; 62967 MW; ED072344033AC530 CRC64;

Query Match 35.3%; Score 508; DB 2; Length 573;  
Best Local Similarity 48.4%; Pred. No. 3.2e-28;  
Matches 119; Conservative 18; Mismatches 61; Indels 48; Gaps 6;

QY 13 LLLAOPAMAEVOLVESGGGVPRGSLRLSCAASGFTPDYKMSWYRQAPGKLEWVSG 72  
Db 10 LLLAALKGVQCEVQGVESGGGLVQGRSLRLSCAASGFTPDYAMHWYRQAPGKLEWVSG 69  
QY 73 INNNGSGTYADSVYKGRFTISRDAKNSLYIQOMSLRAEDTAVYYCARMRAPV----- 125  
Db 70 ISMWSGSIQYADSVYKGRFTISRDAKNSLYIQOMSLRAEDTAVYYCARMRAPV----- 129  
QY 126 --IWGQCTLVTVSRGGSGGGGGGGSSSLTQDPAVSVL-----GQTVRITC-- 173

Db 130 MDVWGGQTVTV-----SSAPFKAPDVFPPIISGCRHPKDNSPVILACLI 173  
QY 174 QGDSLSRYASWYQOKRQAPVLYIKNNRPS-GIPDRPSSSGSGNTASLTITGAQABD 232  
Db 174 TGIHPTISVTVTWI-----GTGQSPQRTPEIRKRSYWTSSQLSTPLQOMR 221  
QY 233 EADYYC 238  
Db 222 QGEYKC 227

Search completed: April 25, 2005, 20:34:00  
Job time : 145.106 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 25, 2005, 19:56:06 / Search time 150.818 Seconds  
(without alignments)  
630.846 Million cell updates/sec

Title: US-10-029-926d-208

Perfect score: 1303  
Sequence: 1 MEVQLVESGGGVVRRPGSLR.....VVFGGTKLVLDGGGCKAK 246

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

A: Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1303	100.0	246	5	ABG78329 Human Fv
2	1303	100.0	246	5	ABG92026 Antibody
3	1273	97.7	256	5	ABG78334 Human Fv
4	1273	97.7	256	5	ABG92025 Antibody
5	1260.5	96.7	277	5	ABG92020 Human ant
6	1257	96.5	277	5	ABG78150 Human Fv
7	1257	96.5	277	5	ABG91841 Human ant
8	1253	96.2	277	8	AD128365 Human scf
9	1233	94.6	277	5	ABG78328 Human Fv
10	1233	94.6	277	5	ABG92019 Human ant
11	1218.5	93.5	239	5	ABP44926 Human Bly
12	1218.5	93.5	239	7	ADG95753 Single ch
13	1214.5	93.2	278	8	AD128367 Human scf
14	1212.5	93.1	239	5	ABP46027 Human Bly
15	1212.5	93.1	239	7	ADG96854 Single ch
16	1210.5	92.9	280	8	ADJ57363 P-selecti
17	1203.5	92.4	280	8	AD128368 Human scf
18	1191.5	91.4	239	5	ABP46004 Human Bly
19	1191.5	91.4	239	7	ADG96831 Single ch
20	1181	90.6	238	3	AAV95198 Anti-plat
21	1178	90.4	244	6	AAO31135 Human CMO
22	1178	90.4	309	2	AAW83322 Single ch
23	1178	90.4	309	5	ABB09603 Amino aci
24	1178	90.4	309	6	ABG74384 Single ch
25	1178	90.4	309	7	ADG98737 Human sin

#### ALIGNMENTS

RESULT 1	ABG78329	standard; protein; 246 AA.
ID	ABG78329	standard; protein; 246 AA.
XX	ABG78329;	
XX	15-NOV-2002 (first entry)	
DT	15-NOV-2002	
XX	Human Fv molecule hypervariable region related peptide #204.	
XX	Human Fv molecule; hypervariable region; single chain Fv; cytostatic;	
KW	disulfide Fv; defv; scfv; cancer; carcinoma; sarcoma; leukemia; adenoma;	
KW	lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.	
OS	Homo sapiens.	
XX	WO200259264-A2.	
PN	WO200259264-A2.	
XX	01-AUG-2002.	
PD	01-AUG-2002.	
XX	31-DEC-2001; 2001WO-US049440.	
PE	31-DEC-2001; 2001WO-US049440.	
XX	29-DEC-2000; 2000US-00751181.	
PR	29-DEC-2000; 2000US-00751181.	
XX	(BIOT-) BIO-TECHNOLOGY GEN CORP.	
PA	Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;	
XX	Plakatin D, Peretz T;	
PI	WPI; 2002-619166/66.	
DR	Novel peptide/polypeptide for cancer therapy has Fv molecule, construct	
PT	or fragment, or construct of fragment with enhanced binding	
PT	characteristic so as to selectively bind target cell in favor of other	
XX	cells.	
PS	Disclosure; Page 44-45; 232pp; English.	
XX	The invention relates to a peptide or polypeptide comprising an Fv	
XX	molecule, a construct or fragments or a construct of a fragment with	
CC	enhanced binding characteristics which selectively and/or specifically	
CC	binds to a target cell in favour of other cells, where binding is	
CC	primarily determined by a first hypervariable region and Fv is a single	
CC	chain Fv (scfv) or a disulfide Fv (defv). The peptide, optionally in	
CC	association with or attached, coupled, combined, linked or fused to a	
CC	pharmaceutical agent, is useful in the manufacture of a medicament, where	
CC	the medicament has activity against a diseased cell, preferably a cancer	
CC	cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,	

26	1178	90.4	309	8	ADO40446	Ado40446 Human sin
27	1152.5	88.4	260	5	ABG92023	Abg92023 Antibody
28	1149	88.2	242	8	AD158068	Ad158068 Reg IV-sfp
29	1144	87.8	263	5	ABG92024	Abg92024 Antibody
30	1139.5	87.5	239	5	ABP46007	Abp46007 Human Bly
31	1139.5	87.5	239	7	ADG96834	Adg96834 Single ch
32	1133	86.9	244	6	AAO31139	Aao31139 Human CMO
33	1132.5	86.9	239	5	ABP46024	Abp46024 Human Bly
34	1132.5	86.8	239	7	ADG96851	Adg96851 Single ch
35	1131.5	86.8	245	6	AAO31137	Aao31137 Human CMO
36	1131	86.8	252	5	ABP45405	Abp45405 Human Bly
37	1131	86.8	252	7	ADG96232	Adg96232 Single ch
38	1129.5	86.7	243	7	ADG30436	Adg30436 Human GMB
39	1127.5	86.5	243	5	ABP46045	Abp46045 Human Bly
40	1127.5	86.5	243	7	ADG96872	Adg96872 Single ch
41	1126.5	86.5	239	5	ABP46012	Abp46012 Human Bly
42	1126.5	86.5	239	7	ADG96839	Adg96839 Single ch
43	1121	86.0	242	7	ADG30497	Adg30497 Human GMC
44	1119	85.9	240	5	ABP46002	Abp46002 Human Bly
45	1119	85.9	240	7	ADG96829	Adg96829 Single ch



XX (BIOT-) BIO-TECHNOLOGY GEN CORP.  
PA Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;  
PI Plaksin D, Peretz T;  
XX WPI; 2002-619166/66.  
DR  
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
PT or fragment, or construct of fragment with enhanced binding  
PT characteristics so as to selectively bind target cell in favor of other  
PT cells.  
XX  
PS Example 9; Page 90; 232pp; English.  
XX  
CC The invention relates to a peptide or polypeptide comprising an Fv  
CC molecule, a construct or fragments or a construct of a fragment with  
CC enhanced binding characteristics which selectively and/or specifically  
CC binds to a target cell in favour of other cells, where binding is  
CC primarily determined by a first hypervariable region and Fv is a single  
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
CC association with or attached, coupled, combined, linked or fused to a  
CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
CC the medicament has activity against a diseased cell, preferably a cancer  
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
CC composition for use in inhibiting the growth of a diseased or cancer  
CC cell. This sequence represents a human Fv molecule hypervariable region  
CC related peptide of the invention  
XX  
SQ Sequence 256 AA:  
Query Match 97.7%; Score 1273; DB 5; Length 256;  
Best Local Similarity 99.6%; Pred. No. 1.9e-80;  
Matches 241; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEVQLVESGGGVVRRPGSLRLSCAASGFTPDYGMVWVROAPGKLEWVGIMNGSGTG 60  
DB 1 MEVQLVESGGGVVRRPGSLRLSCAASGFTPDYGMVWVROAPGKLEWVGIMNGSGTG 60  
QY 61 YADSVKGRFTISRDNAKNSLYLQNMSLRADTAIVYCARARAPYIWQGTLLVTVSRGGG 120  
DB 61 YADSVKGRFTISRDNAKNSLYLQNMSLRADTAIVYCARARAPYIWQGTLLVTVSRGGG 120  
QY 121 SGGGGSGGGSSSLTQDPAVSVALGQTVRITTCGDSLSRYSYASWYQKPGQAPLVLYYK 180  
DB 121 SGGGGSGGGSSSLTQDPAVSVALGQTVRITTCGDSLSRYSYASWYQKPGQAPLVLYYK 180  
QY 181 NRPSPGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSSGNHVPFGGTLTVLGG 240  
DB 181 NRPSPGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSSGNHVPFGGTLTVLGG 240  
QY 241 GG 242  
DB 241 GG 242  
RESULT 4  
ABG92025  
ID ABG92025 standard; protein; 256 AA.  
XX  
AC ABG92025;  
XX  
DT 04-DEC-2002 (first entry)  
XX  
DE Antibody biotag #1.  
XX  
KM Antibody; antibody biotag; cancer; tumour; cell rolling; inflammation;  
KM metacarcinosis; hypervariable region; autoimmune disease; thrombosis;  
KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
KM myocardial infarction; retinopathic disease; abnormal platelet function;  
KM sulphated tyrosine-dependent protein-protein interaction.

XX Unidentified.  
OS  
XX  
PN WO200253700-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 31-DEC-2001; 2001WO-US049442.  
XX  
PR 29-DEC-2000; 2000US-00751181.  
PR 29-DEC-2000; 2000US-0258948P.  
XX  
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.  
PA Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
PI Stanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;  
XX WPI; 2002-674776/72.  
DR  
XX  
PT Novel isolated epitope present on cancer cells and important in  
PT physiological phenomena such as cell rolling, metastasis and  
PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
PT diseases, and cancer.  
XX  
PS Disclosure; Fig 51; Opp; English.  
XX  
CC The invention relates to an isolated epitope present on cancer cells and  
CC important in physiological phenomena such as cell rolling, metastasis and  
CC inflammation, where the epitope is capable of being bound by an antibody,  
CC its antigen-binding fragment or its complex comprising at least one  
CC antibody or its binding fragment having a first hypervariable region. The  
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
CC mortality of tumour or leukaemia cells, for increasing the susceptibility  
CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
CC leukaemia agents, or for decreasing the number of tumour or leukaemia  
CC cells in a patient, or in the manufacture of a medicament for the above  
CC mentioned purposes. The epitopes are useful for diagnosing and treating  
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
CC retinopathic diseases and other diseases mediated by abnormal platelet  
CC function and diseases caused by sulphated tyrosine-dependent protein-  
CC protein interactions. This sequence represents an antibody biotag used in  
CC the scope of the invention  
XX  
SQ Sequence 256 AA:  
Query Match 97.7%; Score 1273; DB 5; Length 256;  
Best Local Similarity 99.6%; Pred. No. 1.9e-80;  
Matches 241; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEVQLVESGGGVVRRPGSLRLSCAASGFTPDYGMVWVROAPGKLEWVGIMNGSGTG 60  
DB 1 MEVQLVESGGGVVRRPGSLRLSCAASGFTPDYGMVWVROAPGKLEWVGIMNGSGTG 60  
QY 61 YADSVKGRFTISRDNAKNSLYLQNMSLRADTAIVYCARARAPYIWQGTLLVTVSRGGG 120  
DB 61 YADSVKGRFTISRDNAKNSLYLQNMSLRADTAIVYCARARAPYIWQGTLLVTVSRGGG 120  
QY 121 SGGGGSGGGSSSLTQDPAVSVALGQTVRITTCGDSLSRYSYASWYQKPGQAPLVLYYK 180  
DB 121 SGGGGSGGGSSSLTQDPAVSVALGQTVRITTCGDSLSRYSYASWYQKPGQAPLVLYYK 180  
QY 181 NRPSPGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSSGNHVPFGGTLTVLGG 240  
DB 181 NRPSPGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSSGNHVPFGGTLTVLGG 240  
QY 241 GG 242  
DB 241 GG 242

RESULT 5  
 ABG92020 standard; protein; 266 AA.  
 ID ABG92020 standard; protein; 266 AA.  
 AC ABG92020;  
 XX  
 DT 04-DEC-2002 (first entry)  
 DE Human antibody fragment #204.  
 XX  
 KM Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;  
 KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
 KM myocardial infarction; retinopathic disease; abnormal platelet function;  
 KM sulphated tyrosine-dependent protein-protein interaction.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200253700-A2.  
 PD 11-JUL-2002.  
 PF 31-DEC-2001; 2001WO-US049442.  
 PR 29-DEC-2000; 2000US-00751181.  
 PR 29-DEC-2000; 2000US-0258948P.  
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
 PI Santhanon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;  
 PI WPI; 2002-674776/72.  
 DR  
 XX  
 PT Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer.  
 XX  
 PS Disclosure; Page 309-310; Opp; English.  
 XX  
 CC The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility  
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia  
 CC cells in a patient, or in the manufacture of a medicament for the above  
 CC mentioned purposes. The epitopes are useful for diagnosing and treating  
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
 CC diseases, cardiovascular diseases such as myocardial infarction,  
 CC retinopathic diseases and other diseases mediated by abnormal platelet  
 CC function and diseases caused by sulphated tyrosine-dependent protein-  
 CC protein interactions. This sequence represents a human antibody fragment  
 CC of the invention  
 XX  
 SQ Sequence 266 AA;  
 XX  
 Query Match 96.7%; Score 1260.5; DB 5; Length 266;  
 Best Local Similarity 98.4%; Pred. No. 1,4e-79;  
 Matches 241; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 QY 2 EVLVESGGGVRRPGGSLRLSCAASGFTFDYGMKSWRQAPGKGLEWVSGINMGSGTGY 61  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 23 EVLVESGGGVRRPGGSLRLSCAASGFTFDYGMKSWRQAPGKGLEWVSGINMGSGTGY 82  
 QY 62 ADSVKGRFTISRDNAKNSLYLQNNSLRADETAVYVCARARAVIWQGTLYTVSRGGGS 121  
 DB 83 ADSVKGRFTISRDNAKNSLYLQNNSLRADETAVYVCARARAVIWQGTLYTVSRGGGS 142  
 QY 122 GGGGSGGGSSSELTODPAVSVALGQTVRITTCGDSIRSYASWYQKPGQAPFLVITYGN 181  
 DB 143 GGGGSGGGSSSELTODPAVSVALGQTVRITTCGDSIRSYASWYQKPGQAPFLVITYGN 202  
 QY 182 NRPSGIPDRFSGSSSGNTASLTITGQAQADEADYVYNSRSDSGNHVFPGGTKLTVLG 241  
 DB 203 NRPSGIPDRFSGSSSGNTASLTITGQAQADEADYVYNSRSDSGNHVFPGGTKLTVL-CA 261  
 QY 242 GCKAK 246  
 DB 262 AAKAK 266  
 RESULT 6  
 ABG78150 standard; protein; 277 AA.  
 ID ABG78150 standard; protein; 277 AA.  
 AC ABG78150;  
 XX  
 DT 15-NOV-2002 (first entry)  
 DE Human Fv molecule hypervariable region related peptide #25.  
 XX  
 KM Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;  
 KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200259264-A2.  
 PD 01-AUG-2002.  
 PF 31-DEC-2001; 2001WO-US049440.  
 PR 29-DEC-2000; 2000US-00751181.  
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Santhanon E, Levanon A;  
 PI Plaksin D, Peretz T;  
 PI WPI; 2002-619166/66.  
 DR  
 XX  
 PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 PT or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favor of other  
 PT cells.  
 XX  
 PS Claim 4; Page 155-156; 232pp; English.  
 XX  
 CC The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has actively against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention  
 XX

SQ Sequence 277 AA;  
 Query Match 96.5%; Score 1257; DB 5; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 2, 6e-79;  
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVLVESGGGVVRPGGSLRLSCAASGFTFPDYGMVWRQAPGKLEWVSGINNGSGTGY 61  
 DB 23 EVLVESGGGVVRPGGSLRLSCAASGFTFPDYGMVWRQAPGKLEWVSGINNGSGTGY 82  
 QY 62 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMAPYIWGGTLVTVSRGGGGS 121  
 DB 83 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMAPYIWGGTLVTVSRGGGGS 142  
 QY 122 GGGSGGGGSSSELTODPAVSVVALGQTVRITCOGDSLRSYYASWYQOKRGAAPVLYIYGN 181  
 DB 143 GGGSGGGGSSSELTODPAVSVVALGQTVRITCOGDSLRSYYASWYQOKRGAAPVLYIYGN 202  
 QY 182 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNGHVVFGGGTLTVLG 239  
 DB 203 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNGHVVFGGGTLTVLG 260

RESULT 7  
 ABG91841  
 ID ABG91841 standard; protein; 277 AA.  
 AC ABG91841;  
 XX  
 DT 04-DEC-2002 (first entry)  
 XX  
 DE Human antibody fragment #25.  
 XX  
 KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;  
 KW reestenosis; leukaemia; inflammatory disease; cardiovascular disease;  
 KW myocardial infarction; retinopathic disease; abnormal platelet function;  
 KW sulphated tyrosine-dependent protein-protein interaction.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200253700-A2.  
 XX  
 PD 11-JUL-2002.  
 XX  
 PF 31-DEC-2001; 2001WO-US049442.  
 XX  
 PR 29-DEC-2000; 2000US-00751181.  
 PR 29-DEC-2000; 2000US-0258948P.  
 XX  
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 XX  
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;  
 DR WPI; 2002-674776/72.  
 XX  
 PT Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer.  
 XX  
 PS Claim 23; Page 233-234; Opp; English.  
 XX  
 CC The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, reestenosis, metastasis, growth and/or replication of  
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-

CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility  
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia  
 CC cells in a patient, or in the manufacture of a medicament for the above  
 CC mentioned purposes. The epitopes are useful for diagnosing and treating  
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
 CC diseases, cardiovascular diseases such as myocardial infarction,  
 CC retinopathic diseases and other diseases mediated by abnormal platelet  
 CC function and diseases caused by sulphated tyrosine-dependent protein-  
 CC protein interactions. This sequence represents a human antibody fragment  
 CC of the invention

SQ Sequence 277 AA;  
 Query Match 96.5%; Score 1257; DB 5; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 2, 6e-79;  
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVLVESGGGVVRPGGSLRLSCAASGFTFPDYGMVWRQAPGKLEWVSGINNGSGTGY 61  
 DB 23 EVLVESGGGVVRPGGSLRLSCAASGFTFPDYGMVWRQAPGKLEWVSGINNGSGTGY 82  
 QY 62 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMAPYIWGGTLVTVSRGGGGS 121  
 DB 83 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMAPYIWGGTLVTVSRGGGGS 142  
 QY 122 GGGSGGGGSSSELTODPAVSVVALGQTVRITCOGDSLRSYYASWYQOKRGAAPVLYIYGN 181  
 DB 143 GGGSGGGGSSSELTODPAVSVVALGQTVRITCOGDSLRSYYASWYQOKRGAAPVLYIYGN 202  
 QY 182 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNGHVVFGGGTLTVLG 239  
 DB 203 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNGHVVFGGGTLTVLG 260

RESULT 8  
 ADI28366  
 ID ADI28366 standard; protein; 277 AA.  
 AC ADI28366;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Human scFv fragment Y1, binds to platelets.  
 XX  
 KW Human; antibody; scFv; platelet; drug delivery; cancer; therapy.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 XX  
 PN WO2004002528-A1.  
 XX  
 PD 08-JAN-2004.  
 PD  
 PF 30-JUN-2003; 2003WO-US020604.  
 PR 01-JUL-2002; 2002US-00189025.  
 XX  
 PA (SAVI-) SAVIENT PHARM INC.  
 XX  
 PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;  
 DR WPI; 2004-099189/10.  
 XX  
 CC Composition comprising an agent and/or antibody or its fragment, useful  
 CC for treating auto-immune disease, thrombosis, reestenosis, metastasis, or  
 CC for inhibiting growth and/or replication of tumor cells or leukemia  
 CC cells.  
 XX  
 PS Claim 13; SEQ ID NO 1; 58pp; English.  
 XX  
 CC The present sequence is the protein sequence of human scFv fragment Y1.  
 CC This antibody was identified by screening a human antibody phage library

CC that has diversity only in the heavy chain CDR3 regions. Fixed human  
CC platelets were screened in order to identify antibodies that bind  
CC and 285 on glyvocalcin, a subunit of the CD2 complex. Y1 also binds the  
CC N-terminal of PSL-1, a receptor for E-, L- and P-selectins, and has a  
CC high affinity for primary leukaemia cells. The invention relates to  
CC compositions utilising an agent and an antibody or its fragment. The  
CC agent is a toxin, radioisotope or pharmaceutical agent such as  
CC doxorubicin. It is complexed or combined with or conjugated to the  
CC antibody or its fragment. The agent and/or antibody can be present in the  
CC composition as a sub-clinical amount, i.e. less than the amount generally  
CC found to be clinically effective when the agent is administered alone.  
CC The composition is used in claimed methods of: inhibiting cell rolling,  
CC inflammation, thrombosis, restenosis, metastasis, the growth and/or  
CC replication of tumour cells or leukaemia cells, an increase in number of  
CC tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,  
CC platelet-platelet and/or cell-platelet complex formation, aggregation or  
CC adhesion; increasing the mortality rate of tumour or leukaemia cells; the  
CC susceptibility of disease cells to damage by anti-disease agents, and the  
CC susceptibility of tumour or leukaemia cells to damage by anti-cancer  
CC agents; and ameliorating the effects of a disease, preventing a disease,  
CC treating a disease or inhibiting the progress of a disease.

XX  
XX  
SQ Sequence 277 AA:

Query Match 96.2%; Score 1253; DB 8; Length 277;  
Best Local Similarity 99.6%; Pred. No. 4.9e-79;  
Matches 233; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVQLVDSGGGVNPPGSLRLSCAASGFTPDYGMNWRAQPGKLEWVSGINNNGSTGY 61  
DB 23 EVQLVDSGGGVNPPGSLRLSCAASGFTPDYGMNWRAQPGKLEWVSGINNNGSTGY 82  
QY 62 ADSVKGRTTISRMAKNSLYLQNSLRADDTAVYYCARMAPYVWGQGLTVTVSRGGGS 121  
DB 83 ADSVKGRTTISRMAKNSLYLQNSLRADDTAVYYCARMAPYVWGQGLTVTVSRGGGS 142  
QY 122 GGGSGGGGSSSELTQDPAVSVALGQTVRITCGDLSRSYASVYQKPGQAPLVLYYGN 181  
DB 143 GGGSGGGGSSSELTQDPAVSVALGQTVRITCGDLSRSYASVYQKPGQAPLVLYYGN 202  
QY 182 NRPSGIPDRPSSGSSGNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGTYLTVLG 239  
DB 203 NRPSGIPDRPSSGSSGNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGTYLTVLG 260

RESULT 9  
ABG78328  
ID ABG78328 standard; protein; 277 AA.  
XX  
XX

AC ABG78328;  
XX  
XX  
DT 15-NOV-2002 (first entry)  
XX  
XX  
DE Human Fv molecule hypervariable region related peptide #203.

XX Human Fv molecule; hypervariable region; single chain Fv; cytosstatic;  
XX disulfide Fv; dsFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
XX lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.  
XX Homo sapiens.  
XX  
XX  
XX NO200259264-A2.  
XX  
XX  
XX 01-AUG-2002.  
XX  
XX  
XX 31-DEC-2001; 2001WO-US049440.  
XX  
XX  
XX 29-DEC-2000; 2000US-00751181.  
XX  
XX  
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.  
XX  
XX  
XX Hagai Y, Lazarovite J, Guy R, Lipchitz O, Szanton E, Levanon A;

PI Plakelin D, Peretz T;  
XX  
XX  
DR MPI; 2002-619166/66.  
DR N-PSDB; ABS63384.  
XX  
XX

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
PT or fragment, or construct of fragment with enhanced binding  
PT characteristics so as to selectively bind target cell in favor of other  
PT cells.

XX  
XX  
PS Claim 141; Fig 14; 232pp; English.

XX  
XX  
CC The invention relates to a peptide or polypeptide comprising an Fv  
CC molecule, a construct or fragments or a construct of a fragment with  
CC enhanced binding characteristics which selectively and/or specifically  
CC binds to a target cell in favour of other cells, where binding is  
CC primarily determined by a first hypervariable region and Fv is a single  
CC chain Fv (dsFv) or a disulfide Fv (dsFv). The peptide, optionally in  
CC association with or attached, coupled, combined, linked or fused to a  
CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
CC the medicament has activity against a diseased cell, preferably a cancer  
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
CC composition for use in inhibiting the growth of a diseased or cancer  
CC cell. This sequence represents a human Fv molecule hypervariable region  
CC related peptide of the invention

XX  
XX  
SQ Sequence 277 AA:

Query Match 94.6%; Score 1233; DB 5; Length 277;  
Best Local Similarity 97.9%; Pred. No. 1.2e-77;  
Matches 233; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EVQLVDSGGGVNPPGSLRLSCAASGFTPDYGMNWRAQPGKLEWVSGINNNGSTGY 61  
DB 23 EVQLVDSGGGVNPPGSLRLSCAASGFTPDYGMNWRAQPGKLEWVSGINNNGSTGY 82  
QY 62 ADSVKGRTTISRMAKNSLYLQNSLRADDTAVYYCARMAPYVWGQGLTVTVSRGGGS 121  
DB 83 ADSVKGRTTISRMAKNSLYLQNSLRADDTAVYYCARLTHPYWGQGLTVTVSRGGGS 142  
QY 122 GGGSGGGGSSSELTQDPAVSVALGQTVRITCGDLSRSYASVYQKPGQAPLVLYYGN 181  
DB 143 GGGSGGGGSSSELTQDPAVSVALGQTVRITCGDLSRSYASVYQKPGQAPLVLYYGN 202  
QY 182 NRPSGIPDRPSSGSSGNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGTYLTVLG 239  
DB 203 NRPSGIPDRPSSGSSGNTASLTITGAQAEDEADYCNRSRDSGNHVVFGGTYLTVLG 260

RESULT 10  
ABG92019  
ID ABG92019 standard; protein; 277 AA.  
XX  
XX  
AC ABG92019;  
XX  
XX  
DT 04-DEC-2002 (first entry)  
XX  
XX  
DE Human antibody fragment #203.

XX Human antibody; epitope; cancer; tumour; cell rolling; inflammation;  
XX metastasis; hypervariable region; autoimmune disease; thrombosis;  
XX restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
XX myocardial infarction; retinopathic disease; abnormal platelet function;  
XX sulphated tyrosine-dependent protein-protein interaction.  
XX  
XX  
XX Homo sapiens.  
XX  
XX  
XX NO200253700-A2.  
XX  
XX  
XX 11-JUL-2002.  
XX  
XX

Pf		31-DEC-2001; 2001MO-USO494442.
Rr		29-DEC-2000; 2000US-00751181.
Xx		29-DEC-2000; 2000US-0258948P.
Pt	(BIOT-) BIO-TECHNOLOGY GEN CORP.	
Dl	Lazarovite J, Hagek Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;	
Xx	Szathon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;	
Dl	WPJ; 2002-674776/72.	
Pt	Novel isolated epitope present on cancer cells and important in	
Pt	physiological phenomena such as cell rolling, metastasis and	
Pt	Inflammation, for treating autoimmune, inflammatory or cardiovascular	
Pt	diseases, and cancer.	
Cc	Claim 23; Page 308-309; Opp; English.	
Cc	The invention relates to an isolated epitope present on cancer cells and	
Cc	important in physiological phenomena such as cell rolling, metastasis and	
Cc	inflammation, where the epitope is capable of being bound by an antibody,	
Cc	its antigen-binding fragment or its complex comprising at least one	
Cc	antibody or its binding fragment having a first hypervariable region. The	
Cc	epitopes are useful for inhibiting cell rolling, inflammation, autoimmune	
Cc	disease, thrombois, restenosis, metastasis, growth and/or replication of	
Cc	tumour or leukaemia cells, increase in number of tumour or leukaemia	
Cc	cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-	
Cc	platelet and/or cell-platelet adhesion or aggregation, for increasing	
Cc	mortality of tumour or leukaemia cells, for increasing the susceptibility	
Cc	of diseased cells to damage by anti-disease, anti-cancer or anti-	
Cc	leukemia agents, or for decreasing the number of tumour or leukemia	
Cc	cells in a patient, or in the manufacture of a medicament for the above	
Cc	mentioned purposes. The epitopes are useful for diagnosing and treating	
Cc	diseases such as cancer, leukemia, autoimmune diseases, inflammatory	
Cc	diseases, cardiovascular diseases such as myocardial infarction,	
Cc	retinopathic diseases and other diseases mediated by abnormal platelet	
Cc	function and diseases caused by sulphated tyrosine-dependent protein-	
Cc	protein interactions. This sequence represents a human antibody fragment	
Cc	of the invention	
SQ	Sequence 277 AA:	
Query Match	94.6%; Score 1233; DB 5; Length 277;	
Best Local Similarity	97.9%; Pred. No. 1.2e-77;	
Matches 233; Conservative 1; Mismatches 7; Indels 0; Gaps 0.		
Gy	2 EVOLVESSGCGYVRPGSGIRLSCNAGSFFPDYGMWVROAPCKGLEMTVGINMGCSSTGY 61 	
Dd	23 EVOLVESGGGVRRPGSGIRLSGNASGFPPDYGMSWVOAEPKGLMWSGINMGCSSTGY 82 	
Gy	62 ADVSKGRITTSRDNAKNSLIOMNSLRABDPVVVCAMBRAPVINGOGTLVTYSRGGGS 121 	
Dd	83 ADSVKAGRITISRDNANKNLIIOMNSLRABDRIVYCALKTHFPMGGTILTVSRGGGS 142 	
Gy	122 GGGSGGGSSELTDPAVSVALGTQTVAITTCGDLSRSRYVASWYOAKGOAPVLVIYEKN 181 	
Dd	143 GGGSGGGSSELTDDPAVSVALGTQTVAITTCGDLSRSRYVASWYOARKGOAPVLVIYEKN 202 	
Gy	182 NRPESGIPIRFEGSSSGNTASTLTITAQADEADYYCNRDSNGNHVPFGGKTLLTVLG 239 	
Dd	203 NRPSGIPIPRFESSSGNTASTLTITAQADEADYYCNCRSDSNHNVFGGKTLLTVLG 260 	
RESULT 11		
ID	ABP44926 standard; protein; 239 AA.	
XX	ABP44926;	
AC		
DT	19-AUG-2002 (first entry)	
XX		
DB	Human ELys binding scFv SEQ ID 937.	

XX	Blvs; B lymphocyte stimulator; TNF superfamily; human; cytosolic;	
KM	tumour necrosis factor; B cell proliferation; B cell differentiation;	
KM	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;	
KM	antiaids; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;	
KM	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;	
KM	common variable immunodeficiency; acquired immunodeficiency syndrome.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200202641-A1.	
XX		
PD	10-JAN-2002.	
XX		
PF	15-JUN-2001; 2001WO-US019110.	
XX		
PR	16-JUN-2000; 2000US-0212210P.	
PR	17-OCT-2000; 2000US-0240816P.	
PR	16-MAR-2001; 2001US-0276248P.	
PR	21-MAR-2001; 2001US-0277379P.	
PR	25-MAY-2001; 2001US-0293499P.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
PA	(CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.	
XX		
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;	
XX		
DR	WPI; 2002-114799/15.	
XX		
PT	Antibodies against B lymphocyte Stimulating polypeptides, useful for the	
PT	diagnosis and treatment of cancers and immune disorders.	
XX		
PS	Claim 1; Page 1520-1521; 3148pp; English.	
XX		
CC	This invention describes novel antibodies that immunospecifically bind to	
CC	B lymphocyte Stimulator (Blvs) polypeptides. Blvs is a member of the	
CC	tumour necrosis factor (TNF) super family and induces B cell	
CC	proliferation and differentiation. The antibodies of the invention have	
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,	
CC	antirheumatic and antiaids activity and can be used in vaccines to	
CC	inhibit the expression and activity of Blvs. The antibodies bind to Blvs	
CC	and so may be used to detect and quantitate the presence of Blvs in	
CC	biological samples and may be used in this way to diagnose disease	
CC	associated with aberrant expression of Blvs. They may also be	
CC	administered to treat diseases associated with aberrant Blvs expression	
CC	and actively such as cancer, immune, and autoimmune disorders and	
CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,	
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and	
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP4728 represent	
CC	the antibodies and fragments of the antibodies described in the method of	
XX	the invention	
XX		
SQ	Sequence 239 AA:	
QY	Query Match	93.5%; Score 1218.5; DB 5; Length 239;
	Best Local Similarity	97.9%; Pred. No. 1e-76;
	Matches 234; Conservative	0; Mismatches 4; Indels 1; Gaps 1
QY	2	EVOLVESSGGIVRRRGGSRLSCASGFFPDYGSWVRQAPKGLGEMVSGIMWNGSGTGY 61
DB	1	EVOLVESSGGVARRRPGSSRLSCASGFFPDYGSWVRQAPKGLGEMVSGIMWNGSGTGY 60
QY	62	ADVYKGRRTISRDNKNSLYQMSLRBEDPAVYYCABMR-APVIMGGQTLVTVSRGGGG 120
DB	61	ADVYKGRRTISRDNKNSLYQMSLRBEDPAVYYCARRRYALDYMGGQTLVTVSRGGGG 120
QY	121	SGGGSGGGGSSSELTPDPAVSVALGQTVRITCGQDSLRSYYASWYQQRGQAPVLYVYK 180
DB	121	SGGGSGGGGSSSELTPDPAVSVALGQTVRITCGQDSLRSYYASWYQQRGQAPVLYVYK 180
QY	181	NNRPSGIPDRSSGSSSGNTAFLITTGAAQAEADYVYCNRSRBSGHHVYFGGATKLTVLG 239
DB	181	NNRPSGIPDRSSGSSSGNTAFLITTGAAQAEADYVYCNRSRBSGHHVYFGGATKLTVLG 239

## RESULT 12

ADG95753  
ID ADG95753 standard; protein; 239 AA.

AC ADG95753;

DT 11-MAR-2004 (first entry)

DE Single chain antibody that immunospecifically binds Blys SeqID 937.

XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;  
XX B cell proliferation; differentiation; scfv; myaesthesia gravis;  
XX multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;  
XX carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;  
XX antiinflammatory; antiallergic; antiallergic; cytostatic.

OS Unidentified.

PN WO2003055979-A2.

PD 10-JUL-2003.

PF 14-NOV-2002; 2002WO-US036496.

PR 16-NOV-2001; 2001US-0331469P.

PR 19-DEC-2001; 2001US-0340817P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

DR WPI; 2003-505530/47.

PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator  
PT (Blys), useful for detecting and treating diseases or disorders e.g.  
PT rheumatoid arthritis, asthma and leukemia.

PS Example 1; SEQ ID NO 937; 394pp; English.

XX This invention relates to novel antibodies that immunospecifically bind  
XX to B lymphocyte stimulator (Blys). The Blys gene has been mapped to  
XX chromosome 13q34 and encodes a protein that is a member of the tumour  
XX necrosis factor superfamily and induces both in vivo and in vitro B cell  
XX proliferation and differentiation. Specifically, it refers to single  
XX chain antibody molecules (scfvs) derived, preferably, from the variable  
XX heavy CDR3 region that immunospecifically bind to a polypeptide, or  
XX fragment thereof, of either human, murine, rat or monkey Blys. The  
XX present invention refers to the use of such antibodies in various methods  
XX for the detection, diagnosis and prognosis of diseases related to the  
XX aberrant expression or inappropriate function of Blys or its receptor. As  
XX such, these compositions are useful for identifying immune disorders  
XX including myasthenia gravis and multiple sclerosis, inflammatory  
XX disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
XX as AIDS and proliferative disorders including leukaemia, carcinoma and  
XX lymphoma. Accordingly, they can be described as exhibiting various  
XX activities such as antirheumatic, antiarthritic, neuroprotective,  
XX antiinflammatory, antiallergic, antiallergic and cytostatic. This  
XX polypeptide sequence is a single chain antibody that binds Blys of the  
XX invention. NOTE: The sequence data for this patent did not form part of  
XX the printed specification, but was obtained in electronic format  
XX directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 239 AA;

Query Match 93.5%; Score 1218.5; DB 7; Length 239;

Best Local Similarity 97.9%; Pred. No. 1e-76;

Matches 233; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 2 EVOLVESGGGVVPRGSGSLRLSCAASGFTPDYGMKSWRQAPGKGLVIVSGINNGSGTGY 61  
DB 1 EVOLVESGGGVVPRGSGSLRLSCAASGFTPDYGMKSWRQAPGKGLVIVSGINNGSGTGY 60

QY 62 ADSVKGRFTISRDNANSLYLQNNSLRAEDTAVVYCARNR-APVWGGTLVTVSSGGG 120  
DB 61 ADSVKGRFTISRDNANSLYLQNNSLRAEDTAVVYCARRALDYGGGTLVTVSSGGG 120  
QY 121 SGGGSGGGGSGGSGSLTDDPAVSVALGQTVRITCGDSLRYSYASWYQKRGQAPVLYYK 180  
DB 121 SGGGSGGGGSGGSGSLTDDPAVSVALGQTVRITCGDSLRYSYASWYQKRGQAPVLYYK 180  
QY 181 NNRPSTGTPRFGSSSGNTASLTITGAQADEADYVCNSRDSGNNHVFGGGFKLTVLG 239  
DB 181 NNRPSTGTPRFGSSSGNTASLTITGAQADEADYVCNSRDSGNNHVFGGGFKLTVLG 239

## RESULT 13

AD128367  
ID AD128367 standard; protein; 278 AA.

AC AD128367;

DT 06-MAY-2004 (first entry)

DE Human scFv fragment Y17, binds to platelets.

XX Human; antibody; scFv; platelet; drug delivery; cancer; therapy.

XX Homo sapiens.

OS WO2004002528-A1.

PN 08-JAN-2004.

PF 30-JUN-2003; 2003WO-US020604.

PR 01-JUL-2002; 2002US-00189025.

PA (SAVI-) SAVIENT PHARM INC.

PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;

DR WPI; 2004-099189/10.

XX Composition comprising an agent and/or antibody or its fragment, useful  
XX for treating auto-immune disease, thrombosis, restenosis, metastasis, or  
XX for inhibiting growth and/or replication of tumor cells or leukemia  
XX cells.

PS Claim 13; SEQ ID NO 2; 58pp; English.

XX The present sequence is the protein sequence of human scFv fragment Y17.  
XX This antibody was identified by screening a human antibody phage library  
XX that has diversity only in the heavy chain CDR3 regions. Fixed human  
XX platelets were screened in order to identify antibodies that bind  
XX platelets. Y17 binds leukaemic cells. The invention relates to  
XX compositions utilising an agent and an antibody or its fragment. The  
XX agent is a toxin, radioisotope or pharmaceutical agent such as  
XX doxorubicin. It is complexed or combined with or conjugated to the  
XX antibody or its fragment. The agent and/or antibody can be present in the  
XX composition is a sub-clinical amount, i.e. less than the amount generally  
XX found to be clinically effective when the agent is administered alone.  
XX The composition is used in claimed methods of: inhibiting cell rolling,  
XX inflammation, thrombosis, restenosis, metastasis, the growth and/or  
XX replication of tumour cells or leukaemia cells, an increase in number of  
XX tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,  
XX platelet-platelet and/or cell-platelet complex formation, aggregation or  
XX adhesion; increasing the mortality rate of tumour or leukaemia cells; the  
XX susceptibility of disease cells to damage by anti-disease agents, and the  
XX susceptibility of tumour or leukaemia cells to damage by anti-cancer  
XX agents; and ameliorating the effects of a disease, preventing a disease,  
XX treating a disease or inhibiting the progress of a disease.

XX Sequence 278 AA;



Query Match 93.2%; Score 1214.5; DB 8; Length 278;  
 Best Local Similarity 97.5%; Pred. No. 2.3e-76;  
 Matches 233; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 2 EVOLVESGGGVNPPGSLRLSCAASGFTPD-DYGMKWTROAPGKLEWVGIMNGSGTG 60  
 |||||  
 DB 23 EVOLVESGGGVNPPGSLRLSCAASGFTPDLTTPYFVNRQAPGKLEWVGIMNGSGTG 82  
 |||||

QY 61 YADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYICARRAPVINGQGLTVVSRGGGG 120  
 |||||  
 DB 83 YADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYICARRAPVINGQGLTVVSRGGGG 142  
 |||||

QY 121 SGGGSGGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPVLIYVK 180  
 |||||  
 DB 143 SGGGSGGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPVLIYVK 202  
 |||||

QY 181 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVPFGGTRKLTVLG 239  
 |||||  
 DB 203 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVPFGGTRKLTVLG 261  
 |||||

RESULT 14  
 ABP46027  
 ID ABP46027 standard; protein; 239 AA.  
 XX  
 AC ABP46027;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DE Human BlyS binding scFv SEQ ID 2038.  
 XX  
 KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200202641-A1.  
 XX  
 PD 10-JAN-2002;  
 XX  
 PF 15-JUN-2001; 2001WO-US019110.  
 XX  
 PR 16-JUN-2000; 2000US-0212210P.  
 PR 17-OCT-2000; 2000US-0240816P.  
 PR 16-MAR-2001; 2001US-0276248P.  
 PR 21-MAR-2001; 2001US-0272379P.  
 PR 25-MAY-2001; 2001US-0293499P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX  
 DR WPI; 2002-114799/15.  
 XX  
 PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
 PT diagnosis and treatment of cancers and immune disorders.  
 XX  
 PS Claim 1; Page 2830-2831; 3148pp; English.  
 XX  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS  
 CC and so may be used to detect and quantitate the presence of BlyS in  
 CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of BlyS. They may also be  
 CC administered to treat diseases associated with aberrant BlyS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention  
 XX  
 SQ Sequence 239 AA;

Query Match 93.1%; Score 1212.5; DB 5; Length 239;  
 Best Local Similarity 97.5%; Pred. No. 2.7e-76;  
 Matches 233; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 EVOLVESGGGVNPPGSLRLSCAASGFTPDYGMKWTROAPGKLEWVGIMNGSGTG 61  
 |||||  
 DB 1 EVOLVESGGGVNPPGSLRLSCAASGFTPDYGMKWTROAPGKLEWVGIMNGSGTG 60  
 |||||

QY 62 ADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYICARRR-APVINGQGLTVVSRGGGG 120  
 |||||  
 DB 61 ADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYICARRR-APVINGQGLTVVSRGGGG 120  
 |||||

QY 121 SGGGSGGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPVLIYVK 180  
 |||||  
 DB 121 SGGGSGGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPVLIYVK 180  
 |||||

QY 181 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVPFGGTRKLTVLG 239  
 |||||  
 DB 181 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVPFGGTRKLTVLG 239  
 |||||

RESULT 15  
 ADG96854  
 ID ADG96854 standard; protein; 239 AA.  
 XX  
 AC ADG96854;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Single chain antibody that immunospecifically binds BlyS SeqID 2038.  
 XX  
 KW antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;  
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;  
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia;  
 KW carcinoma; lymphoma; antirheumatic; antiallergic; cytostatic;  
 KW antiinflammatory; antiaesthetic; antiallergic; cytostatic.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003055979-A2.  
 XX  
 PD 10-JUL-2003.  
 XX  
 PF 14-NOV-2002; 2002WO-US036496.  
 XX  
 PR 16-NOV-2001; 2001US-0331469P.  
 PR 19-DEC-2001; 2001US-0340817P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;  
 XX  
 DR WPI; 2003-505350/47.  
 XX  
 PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator  
 PT (BlyS), useful for detecting and treating diseases or disorders e.g.  
 PT rheumatoid arthritis, asthma and leukemia.  
 XX  
 PS Example 1; SEQ ID NO 2038; 394pp; English.  
 XX  
 CC This invention relates to novel antibodies that immunospecifically bind  
 CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to

CC chromosome 13q34 and encodes a protein that is a member of the tumour  
CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
CC proliferation and differentiation. Specifically, it refers to single  
CC chain antibody molecules (scFvs) derived, preferably, from the variable  
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
CC fragment thereof, of either human, murine, rat or monkey Blys. The  
CC present invention refers to the use of such antibodies in various methods  
CC for the detection, diagnosis and prognosis of diseases related to the  
CC aberrant expression or inappropriate function of Blys or its receptor. As  
CC such, these compositions are useful for identifying immune disorders  
CC including myasthenia gravis and multiple sclerosis, inflammatory  
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
CC as AIDS and proliferative disorders including leukaemia, carcinoma and  
CC lymphoma. Accordingly, they can be described as exhibiting various  
CC activities such as antirheumatic, antiarthritic, neuroprotective,  
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This  
CC polypeptide sequence is a single chain antibody that binds Blys of the  
CC invention. NOTE: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX  
SQ Sequence 239 AA:

Query Match 93.1%; Score 1212.5; DB 7; Length 239;  
Best Local Similarity 97.5%; Pred. No. 2.7e-76;  
Matches 233; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 EVOLVESGGGVPRPGSLRLSCAASGFTPDYGMWVROAPGKGLEWVSGINMGSTGY 61  
DB 1 EVOLVESGGGVPRPGSLRLSCAASGFTPDYGMWVROAPGKGLEWVSGINMGSTGY 60  
QY 62 ADSVKGKFTISRDNKNSLYLQWNSLRAEDTAVVYCARMR-APYIWGQGLVTVSRGGG 120  
DB 61 ADSVKGKFTISRDNKNSLYLQWNSLRAEDTAVVYCARRRYALDYWGQGLVTVSSGGG 120  
QY 121 SGGGSGGGSSSLTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPVLYYK 180  
DB 121 SGGGSGGGSSSLTQDPAVSVALGQTVRITTCGDSLRSYASWYQKPGQAPVLYYK 180  
QY 181 NNRPSSGIPDRPSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTLVLYG 239  
DB 181 NNRPSSGIPDRPSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTLVLYG 239

Search completed: April 25, 2005, 20:22:30  
Job time : 151.818 secs

27 MAY 1964

Db 100 ADSVKRVTITSRNANSLYLQNNSLRAEDTAVYYCAKILGAGRGWYFDLMGKGTITVTS 159  
Qy 116 RGGGGGGGGGGGGSSSELTODPAVSVALGQTRITTCGDSLRSYASWYQKPGQAPVL 175  
Db 160 SGGGGGGGGGGGGSSSELTODPAVSVALGQTRITTCGDSLRSYASWYQKPGQAPVL 219  
Qy 176 VIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFEGGTUL 235  
Db 220 VIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFEGGTUL 279  
Qy 236 TVLG 239  
Db 280 TVLG 283

## RESULT 2

US-09-079-029-10  
; Sequence 10, Application US/09079029  
; Patent No. 6342369  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camilla W.  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Chuntarapai, Anan  
; APPLICANT: Kim, Kyung J.  
; TITLE OF INVENTION: Apo-2 Receptor  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,029  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1101R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 312 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-09-079-029-10

Query Match 84.3%; Score 1098.5; DB 3; Length 312;  
Best Local Similarity 87.0%; Pred. No. 6,4e-81;  
Matches 214; Conservative 5; Mismatches 18; Indels 9; Gaps 1;

Qy 3 VOLVESGGGVVRPGGSLRLSCAASGFTPDYGMVSWRQAPGKLEWVSGINMGSGTGYA 62  
Db 41 VOLVESGGGLVQPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWVANKKQDSSEKYYV 100  
Qy 63 DSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARMPAVY-----IMQGTLVT 113  
Db 101 DSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARDLKVKYSSSGSGWFPDGRGTTVT 160  
Qy 114 VSRGGGGGGGGGGSSSELTODPAVSVALGQTRITTCGDSLRSYASWYQKPGQAP 173  
Db 161 VSSGGGGGGGGGGSSSELTODPAVSVALGQTRITTCGDSLRSYASWYQKPGQAP 220

Qy 174 VLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFEGGT 233  
Db 221 VLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFEGGT 280  
Qy 234 KLTVLG 239  
Db 281 KLTVLG 286

## RESULT 3

US-09-260-527-1  
; Sequence 1, Application US/09260527A  
; Patent No. 6228599  
; GENERAL INFORMATION:  
; APPLICANT: Knox, J.P.  
; APPLICANT: Mikkelsen, J.D.  
; APPLICANT: Willats, W.G.  
; TITLE OF INVENTION: ANTIBODY  
; FILE REFERENCE: DYOUI9.001AUS  
; CURRENT APPLICATION NUMBER: US/09/260,527A  
; CURRENT FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 280  
; TYPE: PRP  
; ORGANISM: UNKNOWN  
; FEATURE:  
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a  
; OTHER INFORMATION: phage display library known as the Synthetic scFv  
; OTHER INFORMATION: Library (#1) from the Centre for Protein  
; OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.  
; US-09-260-527-1

Query Match 84.1%; Score 1095.5; DB 3; Length 280;  
Best Local Similarity 88.4%; Pred. No. 9,9e-81;  
Matches 213; Conservative 10; Mismatches 15; Indels 3; Gaps 2;

Qy 2 EVOLVESGGGVVRPGGSLRLSCAASGFTPDYGMVSWRQAPGKLEWVSGI--NNMGSGT 59  
Db 23 EVOLVESGGGLVQPGGSLRLSCAASGFTFSNAMSVRQAPGKLEWVGRIRKTDGTT 82  
Qy 60 GYADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR-MRAPYIMGGTILVTVSRGG 118  
Db 83 DYAPAVKGRFTISRDSKNTLYLQMNSLKTEDTAVYYCARKMRKALRMGGTLVTVSRGG 142  
Qy 119 GSGGGGGGGGGSSSELTODPAVSVALGQTRITTCGDSLRSYASWYQKPGQAPVLVY 178  
Db 143 GSGGGGGGGGGSSSELTODPAVSVALGQTRITTCGDSLRSYASWYQKPGQAPVLVY 202  
Qy 179 GKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFEGGTUL 238  
Db 203 GKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFEGGTUL 262  
Qy 239 G 239  
Db 263 G 263

## RESULT 4

US-09-260-527-3  
; Sequence 3, Application US/09260527A  
; Patent No. 6228599  
; GENERAL INFORMATION:  
; APPLICANT: Knox, J.P.  
; APPLICANT: Mikkelsen, J.D.  
; APPLICANT: Willats, W.G.  
; TITLE OF INVENTION: ANTIBODY  
; FILE REFERENCE: DYOUI9.001AUS  
; CURRENT APPLICATION NUMBER: US/09/260,527A  
; CURRENT FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 3.0





```
/ GENERAL INFORMATION:
/ APPLICANT: Kwak, Larry
/ APPLICANT: Birsagyn, Arya
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
/ FILE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
/ FILE REFERENCE: 14014.0316/P
/ CURRENT APPLICATION NUMBER: US/09/646,028
/ CURRENT FILING DATE: 2000-09-12
/ PRIOR APPLICATION NUMBER: 60/077,745
/ PRIOR FILING DATE: 1998-03-12
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 51
/ LENGTH: 348
/ TYPE: PRN
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-51
```

```
Query Match          60.9%; Score 793.5; DB 4; Length 348;
Best Local Similarity 63.9%; Pred. No. 2.7e-56;
Matches 159; Conservative 27; Mismatches 52; Indels 11; Gaps 4;
```

```
QY 1 MEVLVSGGGGVVRPGGSLRLSCAASGFTPDYGMVWRQAPGKLEWVGGINNGSGTG 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 93 LEVQLVLESGGGLVPGSSSLRLSCAASGLTFTSSSAITWRQAPGKLEWVGISFGPTTY 152
QY 61 YADSVKGRFTISRDNAKNSLYLQNSIRAEEDTAVYICARRAPVI---WGQGLTVTV-S 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 153 YADSVKGRFASRDNSKNTVYLQNNINRPNDAVYFCANNQTFCLDNWGQGLTVTVSS 212
QY 116 RGGGSGGGGGGGGGGSG---SELTODPAVSVALGQTVITQGSLSR---SYASWYQKP 169
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 213 RGGGSGGGGGGGGGGSGGVLTQPPSVSAAPGQRTVISTGSRSNIGAGYDVNWYQKFP 272
QY 170 GQAPVLYIVYGNRRPSGIPDRFGSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVF 229
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 273 ETAPKVLIVYNNRRPSGVPRFSGSGKGTSAISLAITQLQEDGTYTCQCNDSLSGMLF 332
QY 230 GGGTGLTVL 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 333 GGGTGLTVL 341
```

```
RESULT 11
US-08-918-148-75
/ Sequence 75, Application US/08918148A
/ Patent No. 6342220
/ GENERAL INFORMATION:
/ APPLICANT: Adams, Camellia
/ APPLICANT: W.
/ APPLICANT: Carter, Paul J.
/ APPLICANT: Fendly, Brian M.
/ APPLICANT: Gurney, Austin L.
/ TITLE OF INVENTION: Agonist Antibodies
/ FILE REFERENCE: P0979
/ CURRENT APPLICATION NUMBER: US/08/918,148A
/ CURRENT FILING DATE: 1997-08-25
/ NUMBER OF SEQ ID NOS: 79
/ SEQ ID NO 75
/ LENGTH: 245
/ TYPE: PRN
/ ORGANISM: artificial
US-08-918-148-75
```

```
Query Match          59.4%; Score 774.5; DB 3; Length 245;
Best Local Similarity 65.1%; Pred. No. 6.1e-55;
Matches 157; Conservative 28; Mismatches 49; Indels 7; Gaps 4;
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```
QY 2 EVQLVSGGGLVPRPGSLRLSCAASGFTPDYGMVWRQAPGKLEWVGGINNGSGTGY 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 EVQLVSGGGLVPRPGSLRLSCAASGFTPDYGMVWRQAPGKLEWVGISFGPTTY 62
```

```
QY 62 ADSVKGRFTISRDNAKNSLYLQNSIRAEEDTAVYICARRM---APVIWGQGLTVTVSRGG 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 ADSVKGRFTISRDNSKNTVYLQNSIRAEEDTAVYICARRMGEADAFDIWGQGLTVTVSSGG 122
QY 119 GSGGGGGGGGGGSS-ELTODPA-VSVALGQTVITQGSLSRYSWYQKPQAPVLV 176
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 GSGGGGGGGGGGSDIVWTQSPSTLSASVGDRAVITCRASBGIVHMLAWYQKPKAPKLL 182
QY 177 IYKNNRPSGIPDRFGSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVVGGGTGLT 236
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 IYKASSLASGAPRFRFGSGSGADFTLITSLQPDDEPATYVC--QOYSNYPILTGGGTGLE 240
QY 237 V 237
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 V 241
```

```
RESULT 12
US-09-138-091A-73
/ Sequence 73, Application US/09138091A
/ Patent No. 6737249
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Adams, Camellia W.
/ APPLICANT: Carter, Paul J.
/ APPLICANT: Fendly, Brian M.
/ APPLICANT: Gurney, Austin L.
/ TITLE OF INVENTION: Agonist Antibodies
/ FILE REFERENCE: 9491-013-27
/ CURRENT APPLICATION NUMBER: US/09/138,091A
/ CURRENT FILING DATE: 1998-08-21
/ PRIOR APPLICATION NUMBER: US 60/056,736
/ PRIOR FILING DATE: 1997-08-22
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 73
/ LENGTH: 245
/ TYPE: PRN
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: single chain antibody (scFv) fragments
US-09-138-091A-73
```

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Query Match          59.4%; Score 774.5; DB 4; Length 245;
Best Local Similarity 65.1%; Pred. No. 6.1e-55;
Matches 157; Conservative 28; Mismatches 49; Indels 7; Gaps 4;
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QY 2 EVQLVSGGGLVPRPGSLRLSCAASGFTPDYGMVWRQAPGKLEWVGGINNGSGTGY 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 EVQLVSGGGLVPRPGSLRLSCAASGFTPDYGMVWRQAPGKLEWVYIISSSGRTIYY 62
QY 62 ADSVKGRFTISRDNAKNSLYLQNSIRAEEDTAVYICARRM---APVIWGQGLTVTVSRGG 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 ADSVKGRFTISRDNSKNTVYLQNSIRAEEDTAVYICARRMGEADAFDIWGQGLTVTVSSGG 122
QY 119 GSGGGGGGGGGGSS-ELTODPA-VSVALGQTVITQGSLSRYSWYQKPQAPVLV 176
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 GSGGGGGGGGGGSDIVWTQSPSTLSASVGDRAVITCRASBGIVHMLAWYQKPKAPKLL 182
QY 177 IYKNNRPSGIPDRFGSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVVGGGTGLT 236
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 IYKASSLASGAPRFRFGSGSGADFTLITSLQPDDEPATYVC--QOYSNYPILTGGGTGLE 240
QY 237 V 237
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 V 241
```

```
RESULT 13
US-08-918-148-76
/ Sequence 76, Application US/08918148A
/ Patent No. 6342220
/ GENERAL INFORMATION:
```

APPLICANT: Adams, Camellia  
APPLICANT: W.  
APPLICANT: Carter, Paul J.  
APPLICANT: Fendly, Brian M.  
APPLICANT: Gurney, Austin L.  
TITLE OF INVENTION: Agonist Antibodies  
FILE REFERENCE: P0979  
CURRENT APPLICATION NUMBER: US/08/918,148A  
CURRENT FILING DATE: 1997-08-25  
NUMBER OF SEQ ID NOS: 79  
SEQ ID NO 76  
LENGTH: 245  
TYPE: PR  
ORGANISM: artificial  
US-08-918-148-76

Query Match 59.2%; Score 771.5; DB 3; Length 245;  
Best Local Similarity 63.2%; Pred. No. 1.1e-54;  
Matches 153; Conservative 31; Mismatches 51; Indels 7; Gaps 4;

QY 2 EVOLVSGGVPVPGSGSLRISCAASGTFPDYGMWVROAPGKLEWVSGINMGSGTGY 61  
DB 3 EVOLVSGGVPVPGSGSLRISCAASGTFPDYGMWVROAPGKLEWVSGINMGSGTGY 62  
QY 62 ADVKGRFTISRDNANKSLYLQNNSLRAEDTAVVYCARMPAPV---IMGGTLVTVSRGG 118  
DB 63 ADVKGRFTISRDNANKSLYLQNNSLRAEDTAVVYCARMPAPV---IMGGTLVTVSRGG 122  
QY 119 GSGGGGGGGGGSS-ELTQDPA-VSVALGQTVRITCGDSLRSYASWYQKRGQAPLV 176  
DB 123 GSGGGGGGGGGSS-ELTQDPA-VSVALGQTVRITCGDSLRSYASWYQKRGQAPLV 182  
QY 177 IYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGT 236  
DB 183 IYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGT 240  
QY 237 VL 238  
DB 241 IL 242

RESULT 14  
US-09-138-091A-74  
Sequence 74; Application US/09138091A  
Patent No. 6737249  
GENERAL INFORMATION:  
APPLICANT: Adams, Camellia W.  
APPLICANT: Carter, Paul J.  
APPLICANT: Fendly, Brian M.  
APPLICANT: Gurney, Austin L.  
TITLE OF INVENTION: Agonist Antibodies  
FILE REFERENCE: 9491-013-27  
CURRENT APPLICATION NUMBER: US/09/138,091A  
CURRENT FILING DATE: 1998-08-21  
PRIOR APPLICATION NUMBER: US 60/056,736  
PRIORITY FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 74  
LENGTH: 245  
TYPE: PR  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: single chain antibody (scFv) fragments  
US-09-138-091A-74

Query Match 59.2%; Score 771.5; DB 4; Length 245;  
Best Local Similarity 63.2%; Pred. No. 1.1e-54;  
Matches 153; Conservative 31; Mismatches 51; Indels 7; Gaps 4;  
QY 2 EVOLVSGGVPVPGSGSLRISCAASGTFPDYGMWVROAPGKLEWVSGINMGSGTGY 61  
DB 3 EVOLVSGGVPVPGSGSLRISCAASGTFPDYGMWVROAPGKLEWVSGINMGSGTGY 62

QY 62 ADVKGRFTISRDNANKSLYLQNNSLRAEDTAVVYCARMPAPV---IMGGTLVTVSRGG 118  
DB 63 ADVKGRFTISRDNANKSLYLQNNSLRAEDTAVVYCARMPAPV---IMGGTLVTVSRGG 122  
QY 119 GSGGGGGGGGGSS-ELTQDPA-VSVALGQTVRITCGDSLRSYASWYQKRGQAPLV 176  
DB 123 GSGGGGGGGGGSS-ELTQDPA-VSVALGQTVRITCGDSLRSYASWYQKRGQAPLV 182  
QY 177 IYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGT 236  
DB 183 IYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGT 240  
QY 237 VL 238  
DB 241 IL 242

RESULT 15  
US-08-918-148-78  
Sequence 78; Application US/08918148A  
Patent No. 6342220  
GENERAL INFORMATION:  
APPLICANT: Adams, Camellia  
APPLICANT: W.  
APPLICANT: Carter, Paul J.  
APPLICANT: Fendly, Brian M.  
APPLICANT: Gurney, Austin L.  
TITLE OF INVENTION: Agonist Antibodies  
FILE REFERENCE: P0979  
CURRENT APPLICATION NUMBER: US/08/918,148A  
CURRENT FILING DATE: 1997-08-25  
NUMBER OF SEQ ID NOS: 79  
SEQ ID NO 78  
LENGTH: 245  
TYPE: PR  
ORGANISM: artificial  
FEATURE:  
NAME/KEY: unknown  
LOCATION: 208  
OTHER INFORMATION: unknown amino acid  
US-08-918-148-78

Query Match 59.0%; Score 768.5; DB 3; Length 245;  
Best Local Similarity 63.5%; Pred. No. 1.9e-54;  
Matches 153; Conservative 29; Mismatches 52; Indels 7; Gaps 4;

QY 2 EVOLVSGGVPVPGSGSLRISCAASGTFPDYGMWVROAPGKLEWVSGINMGSGTGY 61  
DB 3 EVOLVSGGVPVPGSGSLRISCAASGTFPDYGMWVROAPGKLEWVSGINMGSGTGY 62  
QY 62 ADVKGRFTISRDNANKSLYLQNNSLRAEDTAVVYCARMPAPV---IMGGTLVTVSRGG 118  
DB 63 ADVKGRFTISRDNANKSLYLQNNSLRAEDTAVVYCARMPAPV---IMGGTLVTVSRGG 122  
QY 119 GSGGGGGGGGGSS-ELTQDPA-VSVALGQTVRITCGDSLRSYASWYQKRGQAPLV 176  
DB 123 GSGGGGGGGGGSS-ELTQDPA-VSVALGQTVRITCGDSLRSYASWYQKRGQAPLV 182  
QY 177 IYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGT 236  
DB 183 IYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFGGT 240  
QY 237 V 237  
DB 241 I 241

Search completed: April 25, 2005, 21:12:15  
Job time : 38.9091 secs



GenCore version 5.1.6  
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OM protein - protein search, using BW model

Run on: April 25, 2005, 20:22:46 ; Search time 108.818 Seconds  
(without alignments)  
752.325 Million cell updates/sec

Title: US-10-029-926D-208

Perfect score: 1303

Sequence: 1 MEQVLVESGGGVVPGGSLR.....VVEGGGKTLVLGGGCKAK 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubppa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep:\*

5: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubppa/US09\_NEW\_PUB.pep:\*

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11: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*

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13: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*

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16: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/2/pubppa/US10\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubppa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1260.5	96.7	266	US-10-032-037B-204	Sequence 204, App
2	1260.5	96.7	266	US-10-029-988B-204	Sequence 204, App
3	1260.5	96.7	266	US-10-032-423A-204	Sequence 204, App
4	1257	96.5	277	US-10-032-037B-25	Sequence 25, App1
5	1257	96.5	277	US-10-029-988B-25	Sequence 25, App1
6	1257	96.5	277	US-10-032-423A-25	Sequence 25, App1
7	1257	96.5	277	US-10-029-926B-25	Sequence 25, App1
8	1233	94.6	277	US-10-032-037B-203	Sequence 203, App
9	1233	94.6	277	US-10-029-988B-203	Sequence 203, App
10	1233	94.6	277	US-10-032-423A-203	Sequence 203, App
11	1233	94.6	277	US-10-029-926B-203	Sequence 203, App
12	1218.5	93.5	239	US-09-880-748-937	Sequence 937, App
13	1218.5	93.5	239	US-10-293-418-937	Sequence 937, App

14	1212.5	93.1	239	US-09-880-748-2038	Sequence 2038, App
15	1212.5	93.1	239	US-10-293-418-2038	Sequence 2038, App
16	1205.5	92.5	280	US-10-880-922-6	Sequence 6, App1
17	1196.5	91.8	280	US-10-880-922-5	Sequence 5, App1
18	1196.5	91.8	280	US-10-880-922-56	Sequence 56, App1
19	1195.5	91.7	280	US-10-880-922-60	Sequence 60, App1
20	1192.5	91.5	280	US-10-880-922-61	Sequence 61, App1
21	1191.5	91.4	239	US-09-880-748-2015	Sequence 2015, App
22	1191.5	91.4	239	US-10-293-418-2015	Sequence 2015, App
23	1191.5	91.4	280	US-10-880-922-55	Sequence 55, App1
24	1178	90.4	244	US-10-322-673-42	Sequence 42, App1
25	1178	90.4	309	US-10-052-798-9	Sequence 9, App1
26	1178	90.4	309	US-10-288-917-9	Sequence 9, App1
27	1178	90.4	309	US-10-423-448-9	Sequence 9, App1
28	1139.5	87.5	239	US-09-880-748-2018	Sequence 2018, App
29	1139.5	87.5	239	US-10-293-418-2018	Sequence 2018, App
30	1133	87.0	244	US-10-322-673-45	Sequence 45, App1
31	1132.5	86.9	239	US-09-880-748-2035	Sequence 2035, App
32	1132.5	86.9	239	US-10-293-418-2035	Sequence 2035, App
33	1131.5	86.8	245	US-10-322-673-43	Sequence 43, App1
34	1131	86.8	252	US-09-880-748-1416	Sequence 1416, App
35	1131	86.8	252	US-10-293-418-1416	Sequence 1416, App
36	1129.5	86.7	243	US-10-935-290-69	Sequence 69, App1
37	1127.5	86.5	243	US-09-880-748-2056	Sequence 2056, App
38	1127.5	86.5	243	US-10-293-418-2056	Sequence 2056, App
39	1126.5	86.5	239	US-09-880-748-2023	Sequence 2023, App
40	1126.5	86.5	239	US-10-293-418-2023	Sequence 2023, App
41	1121	86.0	242	US-10-935-290-130	Sequence 130, App
42	1119	85.9	240	US-09-880-748-2013	Sequence 2013, App
43	1119	85.9	240	US-10-293-418-2013	Sequence 2013, App
44	1117.5	85.8	247	US-09-880-748-996	Sequence 996, App
45	1117.5	85.8	247	US-10-293-418-996	Sequence 996, App

#### ALIGNMENTS

RESULT 1

US-10-032-037B-204

Sequence 204, Application US/10032037B

Publication No. US2004001822A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

TITLE OF INVENTION: MOLETTIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

FILE REFERENCE: 10793/44

CURRENT APPLICATION NUMBER: US/10/032,037B

CURRENT FILING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 204

LENGTH: 266

TYPE: PRT

ORGANISM: Homo sapiens

US-10-032-037B-204

Query Match	96.7%	Score 1260.5	DB 15	Length 266
Best Local Similarity	98.4%	Pred. No. 2.4e-82		
Matches 241	Conservative 0	Mismatches 3	Indels 1	Gaps 1
QY	2	EVQLVSGGCVVAPGGSLRISCAASGFTPDYMSVVRQAPGKGLVMSGIMNGSGTGY 61		
DB	23	EVQLVSGGCVVAPGGSLRISCAASGFTPDYMSVVRQAPGKGLVMSGIMNGSGTGY 82		
QY	62	ADSVKRFITSRNNAKNSLYLQWNSYRAEDTAVYYCARRAPIYWGQGLTVTSRGGGGS 121		
DB	83	ADSVKRFITSRNNAKNSLYLQWNSYRAEDTAVYYCARRAPIYWGQGLTVTSRGGGGS 142		
QY	122	GGGSGGGGSSSETLQPAVVALGQTVRITTCQDLSRSYASVYQKPGQAPLVLYGN 181		
DB	143	GGGSGGGGSSSETLQPAVVALGQTVRITTCQDLSRSYASVYQKPGQAPLVLYGN 202		

QY 182 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVLGGG 241  
| | | | |  
Db 203 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVL-GA 261  
| | | | |  
QY 242 GCKAK 246  
| | |  
Db 262 AAKAK 266  
| | |  
RESULT 2  
US-10-029-988B-204  
; Sequence 204, Application US/10029988B  
; Publication No. US20040001839A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/46  
; CURRENT APPLICATION NUMBER: US/10/029,988B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 204  
; LENGTH: 266  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-029-988B-204

Query Match 96.7%; Score 1260.5; DB 15; Length 266;  
Best Local Similarity 98.4%; Pred. No. 2.4e-82;  
Matches 241; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 2 EVOLVESGGGVNRPVPGGSLRLSCAASGFTPDYGMVWROAPGKLEWVSGINMGSTGY 61  
| | | | |  
Db 23 EVOLVESGGGVNRPVPGGSLRLSCAASGFTPDYGMVWROAPGKLEWVSGINMGSTGY 82  
| | | | |  
QY 62 ADSVKGRFTISRDNANKSLYLQWNSLRAEDTAVYYCARMAPYIWGGTLTVYSRGGGGS 121  
| | | | |  
Db 83 ADSVKGRFTISRDNANKSLYLQWNSLRAEDTAVYYCARMAPYIWGGTLTVYSRGGGGS 142  
| | | | |  
QY 122 GGGSGGGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYASWYQKPGQAPVLYIGKN 181  
| | | | |  
Db 143 GGGSGGGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYASWYQKPGQAPVLYIGKN 202  
| | | | |  
QY 182 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVLGGG 241  
| | | | |  
Db 203 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVL-GA 261  
| | | | |  
QY 242 GCKAK 246  
| | |  
Db 262 AAKAK 266  
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RESULT 3  
US-10-032-423A-204  
; Sequence 204, Application US/10032423A  
; Publication No. US20040002450A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/45  
; CURRENT APPLICATION NUMBER: US/10/032,423A  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 12/29/2000  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 204  
; LENGTH: 266

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-423A-204  
Query Match 96.7%; Score 1260.5; DB 15; Length 266;  
Best Local Similarity 98.4%; Pred. No. 2.4e-82;  
Matches 241; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 2 EVOLVESGGGVNRPVPGGSLRLSCAASGFTPDYGMVWROAPGKLEWVSGINMGSTGY 61  
| | | | |  
Db 23 EVOLVESGGGVNRPVPGGSLRLSCAASGFTPDYGMVWROAPGKLEWVSGINMGSTGY 82  
| | | | |  
QY 62 ADSVKGRFTISRDNANKSLYLQWNSLRAEDTAVYYCARMAPYIWGGTLTVYSRGGGGS 121  
| | | | |  
Db 83 ADSVKGRFTISRDNANKSLYLQWNSLRAEDTAVYYCARMAPYIWGGTLTVYSRGGGGS 142  
| | | | |  
QY 122 GGGSGGGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYASWYQKPGQAPVLYIGKN 181  
| | | | |  
Db 143 GGGSGGGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYASWYQKPGQAPVLYIGKN 202  
| | | | |  
QY 182 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVLGGG 241  
| | | | |  
Db 203 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVL-GA 261  
| | | | |  
QY 242 GCKAK 246  
| | |  
Db 262 AAKAK 266  
| | |

RESULT 4  
US-10-032-037B-25  
; Sequence 25, Application US/10032037B  
; Publication No. US20040001822A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/44  
; CURRENT APPLICATION NUMBER: US/10/032,037B  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: 60/258,948  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-037B-25

Query Match 96.5%; Score 1257; DB 15; Length 277;  
Best Local Similarity 100.0%; Pred. No. 4.5e-82;  
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 EVOLVESGGGVNRPVPGGSLRLSCAASGFTPDYGMVWROAPGKLEWVSGINMGSTGY 61  
| | | | |  
Db 23 EVOLVESGGGVNRPVPGGSLRLSCAASGFTPDYGMVWROAPGKLEWVSGINMGSTGY 82  
| | | | |  
QY 62 ADSVKGRFTISRDNANKSLYLQWNSLRAEDTAVYYCARMAPYIWGGTLTVYSRGGGGS 121  
| | | | |  
Db 83 ADSVKGRFTISRDNANKSLYLQWNSLRAEDTAVYYCARMAPYIWGGTLTVYSRGGGGS 142  
| | | | |  
QY 122 GGGSGGGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYASWYQKPGQAPVLYIGKN 181  
| | | | |  
Db 143 GGGSGGGGSSSELTQDPAVSVALGQTVRITCGQDSLRSYASWYQKPGQAPVLYIGKN 202  
| | | | |  
QY 182 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVLGG 239  
| | | | |  
Db 203 NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVFSGGTCLTVLGG 260  
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RESULT 5  
US-10-029-988B-25

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; Sequence 25, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-25
```

```
Query Match          96.5%; Score 1257; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 4.5e-82;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 EVOLVESGGGVPRPGSGLRLSCAASGFTPDYGMWVRQAPGKLEWVSGINMGSGTGY 61
DB 23 EVOLVESGGGVPRPGSGLRLSCAASGFTPDYGMWVRQAPGKLEWVSGINMGSGTGY 82
QY 62 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMPAPVYWGGTILVTYSRGGGGS 121
DB 83 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMPAPVYWGGTILVTYSRGGGGS 142
QY 122 GGGSGGGGSSSELTODPAVSVALGQTVRITCOGDSLSRYASWYQKRGQAPVLVIYGN 181
DB 143 GGGSGGGGSSSELTODPAVSVALGQTVRITCOGDSLSRYASWYQKRGQAPVLVIYGN 202
QY 182 NRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGGTKLTVLG 239
DB 203 NRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGGTKLTVLG 260
```

```
RESULT 6
US-10-032-423A-25
; Sequence 25, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-25
```

```
Query Match          96.5%; Score 1257; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 4.5e-82;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 EVOLVESGGGVPRPGSGLRLSCAASGFTPDYGMWVRQAPGKLEWVSGINMGSGTGY 61
DB 23 EVOLVESGGGVPRPGSGLRLSCAASGFTPDYGMWVRQAPGKLEWVSGINMGSGTGY 82
QY 62 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMPAPVYWGGTILVTYSRGGGGS 121
DB 83 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMPAPVYWGGTILVTYSRGGGGS 142
```

```
QY 122 GGGSGGGGSSSELTODPAVSVALGQTVRITCOGDSLSRYASWYQKRGQAPVLVIYGN 181
DB 143 GGGSGGGGSSSELTODPAVSVALGQTVRITCOGDSLSRYASWYQKRGQAPVLVIYGN 202
QY 182 NRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGGTKLTVLG 239
DB 203 NRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGGTKLTVLG 260
```

```
RESULT 7
US-10-029-926B-25
; Sequence 25, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-25
```

```
Query Match          96.5%; Score 1257; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 4.5e-82;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 EVOLVESGGGVPRPGSGLRLSCAASGFTPDYGMWVRQAPGKLEWVSGINMGSGTGY 61
DB 23 EVOLVESGGGVPRPGSGLRLSCAASGFTPDYGMWVRQAPGKLEWVSGINMGSGTGY 82
QY 62 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMPAPVYWGGTILVTYSRGGGGS 121
DB 83 ADSVKGRFTISRDNANKSLYLQNMNSLRAEDTAVYYCARMPAPVYWGGTILVTYSRGGGGS 142
QY 122 GGGSGGGGSSSELTODPAVSVALGQTVRITCOGDSLSRYASWYQKRGQAPVLVIYGN 181
DB 143 GGGSGGGGSSSELTODPAVSVALGQTVRITCOGDSLSRYASWYQKRGQAPVLVIYGN 202
QY 182 NRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGGTKLTVLG 239
DB 203 NRPSGIPDRFSSGSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGGTKLTVLG 260
```

```
RESULT 8
US-10-032-037B-203
; Sequence 203, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-203
```

```
Query Match          94.6%; Score 1233; DB 15; Length 277;
Best Local Similarity 97.3%; Pred. No. 2.3e-80;
```



```
; Sequence 937, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 937
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-937

Query Match          93.5%; Score 1218.5; DB 10; Length 239;
Best Local Similarity 97.9%; Pred. No. 2.2e-79;
Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 2 EVOLVESGGGVNRPGGSLRLSCAASGFTFDYGMWVROAPGKLEWVSGINMGSGTGY 61
DB 1 EVOLVESGGGVNRPGGSLRLSCAASGFTFDYGMWVROAPGKLEWVSGINMGSGTGY 60
QY 62 ADSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCARMR-APYIWQGTLVTVSRGGG 120
DB 61 ADSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCARRRYALDYWGQGLTVTVSRGGG 120
QY 121 SGGGSGGGSSSELTQDPAVSVALGQTVRTTCQDSLSRYSYASWYQKPGQAPLVLYYK 180
DB 121 SGGGSGGGSSSELTQDPAVSVALGQTVRTTCQDSLSRYSYASWYQKPGQAPLVLYYK 180
QY 181 NNRPISGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTLTVLG 239
DB 181 NNRPISGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTLTVLG 239

RESULT 13
US-10-293-418-937
; Sequence 937, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
```

```
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 937
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-937

Query Match          93.5%; Score 1218.5; DB 15; Length 239;
Best Local Similarity 97.9%; Pred. No. 2.2e-79;
Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 2 EVOLVESGGGVNRPGGSLRLSCAASGFTFDYGMWVROAPGKLEWVSGINMGSGTGY 61
DB 1 EVOLVESGGGVNRPGGSLRLSCAASGFTFDYGMWVROAPGKLEWVSGINMGSGTGY 60
QY 62 ADSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCARMR-APYIWQGTLVTVSRGGG 120
DB 61 ADSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCARRRYALDYWGQGLTVTVSRGGG 120
QY 121 SGGGSGGGSSSELTQDPAVSVALGQTVRTTCQDSLSRYSYASWYQKPGQAPLVLYYK 180
DB 121 SGGGSGGGSSSELTQDPAVSVALGQTVRTTCQDSLSRYSYASWYQKPGQAPLVLYYK 180
QY 181 NNRPISGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTLTVLG 239
DB 181 NNRPISGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTLTVLG 239

RESULT 14
US-09-880-748-2038
; Sequence 2038, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2038
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2038

Query Match          93.1%; Score 1212.5; DB 10; Length 239;
Best Local Similarity 97.5%; Pred. No. 5.9e-79;
Matches 233; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 EVOLVESGGGVNRPGGSLRLSCAASGFTFDYGMWVROAPGKLEWVSGINMGSGTGY 61
DB 1 EVOLVESGGGVNRPGGSLRLSCAASGFTFDYGMWVROAPGKLEWVSGINMGSGTGY 60
QY 62 ADSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCARMR-APYIWQGTLVTVSRGGG 120
DB 61 ADSVKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCARRRYALDYWGQGLTVTVSRGGG 120
QY 121 SGGGSGGGSSSELTQDPAVSVALGQTVRTTCQDSLSRYSYASWYQKPGQAPLVLYYK 180
DB 121 SGGGSGGGSSSELTQDPAVSVALGQTVRTTCQDSLSRYSYASWYQKPGQAPLVLYYK 180
QY 181 NNRPISGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTLTVLG 239
```

DB 181 NNRPSCGIPDRFSSSSGNTASLTITGQAEDBADYYCNSRSDSSGNHVFFGGTTLTVLG 239

RESULT 15  
US-10-293-418-2038  
; Sequence 2038, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2038  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-2038

Query Match 93.1%; Score 1212.5; DB 15; Length 239;  
Best Local Similarity 97.5%; Pred. No. 5.9e-79;  
Matches 233; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
QY 2 EVOLVESGGGVVRPGGSLRLSCAASGFTPDYGMSTWROAPGKGLEWVSGINNGSGTGY 61  
DB 1 EVOLVESGGGVVRPGGSLRLSCAASGFTPDYGMSTWROAPGKGLEWVSGINNGSGTGY 60  
QY 62 ADSVKGRFTISRDAKNSLTLDKNSLRADTAIVYYCARMR-APYIWGQGLTVTVSRGGG 120  
DB 61 ADSVKGRFTISRDAKNSLTLDKNSLRADTAIVYYCARRRYALDYWGQGLTVTVSSGGG 120  
QY 121 SGGGSGGGSSSELTDPAAVVALGQTVRIITCGDSLRSYYASWYQKPGQAPLVLYYK 180  
DB 121 SGGGSGGGSSSELTDPAAVVALGQTVRIITCGDSLRSYYASWYQKPGQAPLVLYYK 180  
QY 181 NNRPSCGIPDRFSSSSGNTASLTITGQAEDBADYYCNSRSDSSGNHVFFGGTTLTVLG 239  
DB 181 NNRPSCGIPDRFSSSSGNTASLTITGQAEDBADYYCNSRSDSSGNHVFFGGTTLTVLG 239

Search completed: April 25, 2005, 21:09:49  
Job time : 109.818 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 25, 2005, 19:57:16 ; Search time 28.3636 Seconds

(Without alignments)  
834.495 Million cell updates/sec

Title: US-10-029-926D-208

Perfect score: 1303

Sequence: 1 MEVQLVESGGGVVRRPGSRLR.....VVFGGTKLTVLGSGGCKAK 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	577	44.3	268	A56446	Ig heavy chain V r
2	568	43.6	109	S19663	Ig lambda chain V
3	562	43.1	108	S47184	Ig lambda chain -
4	561.5	43.1	249	S41374	single chain Fv an
5	551.5	42.3	110	S36272	Ig lambda chain V
6	546	41.9	137	S70444	Ig lambda chain pr
7	541	41.5	108	S38498	Ig lambda chain -
8	539	41.4	109	S38496	Ig lambda chain -
9	530	40.7	233	S25748	Ig lambda chain -
10	527	40.4	108	L3HUSH	Ig lambda chain V-
11	522.5	40.1	233	JC5322	p53 specific singl
12	518.5	39.8	110	S19672	Ig lambda chain V-
13	517.5	39.7	146	S02083	Ig lambda chain V-
14	513	39.4	98	S26928	Ig heavy chain V r
15	510.5	39.2	128	S31595	Ig heavy chain V r
16	503	38.6	96	S36060	Ig lambda chain -
17	503	38.6	115	S13726	Ig lambda chain V
18	502	38.5	121	S31118	Ig heavy chain - h
19	502	38.5	123	S30532	Ig heavy chain V r
20	502	38.5	233	S25741	Ig lambda chain -
21	501	38.4	121	S31104	Ig heavy chain (su
22	495.5	38.0	112	PH1654	Ig heavy chain V r
23	491	37.7	120	S36273	Ig heavy chain V r
24	488	37.5	134	S31699	Ig heavy chain V r
25	487	37.4	138	S31666	Ig heavy chain V r
26	485.5	37.3	120	S44111	Ig heavy chain V-D
27	485.5	37.3	145	S11239	Ig heavy chain V r
28	485	37.2	119	S31108	Ig heavy chain - h
29	485	37.2	160	S05271	Ig heavy chain pre

30	484.5	37.2	120	S48798	Ig heavy chain V r
31	482	37.0	119	S31107	Ig heavy chain - h
32	480	36.8	121	I55673	Ig heavy chain - h
33	480	36.8	123	S31114	Ig heavy chain - h
34	478	36.7	119	D36005	Ig heavy chain V r
35	477	36.6	140	S31686	Ig heavy chain V r
36	476	36.5	119	S36005	Ig heavy chain V r
37	475	36.5	139	S37781	Ig variable region
38	473.5	36.3	124	S20782	Ig heavy chain V r
39	473.5	36.3	128	S26790	Ig heavy chain V r
40	473.5	36.3	140	S70442	Ig heavy chain pre
41	473.5	36.3	151	A60943	Ig heavy chain pre
42	473	36.3	127	S38489	Ig heavy chain - h
43	472	36.3	135	S31598	Ig heavy chain V r
44	472	36.2	98	S26927	Ig heavy chain V r
45	472	36.2	143	S23524	Ig heavy chain V r

## ALIGNMENTS

## RESULT 1

A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence\_reviseion 19-Jan-1996 #text\_change 16-Aug-1996

C/Accession: A56446

R/Ting, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident

A/Reference number: A56446; PMID:95229583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TDN>

A/Cross-references: GB:U20617

C/Keywords: heterotetramer; immunoglobulin

Query Match 44.3%; Score 577; DB 2; Length 268;

Best Local Similarity 50.2%; Pred. No. 1.3e-32;

Matches 121; Conservative 34; Mismatches 78; Indels 8; Gaps 5;

QY	2	EVQLVESGGGVVRRPGSRLRCAASGFTPDYGMWVRQAPGKLEWISINNCGSTGY	61
DB	3	QVQLQSSGAEIVRPGASVYKLSCTTSGFNITDITMHWKQRPBGLEIGRIAPANGITKY	62
QY	62	ADSVKGRFTISRDNANKSLYLQNSLRRAEDTAVYYCAR--MRAPVWGGLVTVSRGG	118
DB	63	DPKFGKATIAVDTSNTAVLQSLTSBEDTAVYYCASVYLTREYENWVGQTVTVSSGG	122
QY	119	GGSGGGSGSGGGSGS-ELTQDPVAV-SVALGQTVAITQGSLSRYSVSWYQKQCAPVYV	176
DB	123	GGSGGGDSGGGSDIELTQSPALMSASLGKVTMSGRASSVA-FITWYQKQKDAAPKWL	181
QY	177	IYQNNRPSGIPRPFSSSSGNTASLTITGAQAEADENACNRRDSSGNHVFVGGTKLT	236
DB	182	VYTSHPFQVPAVRFSGSGSGNSYLTISMEGEDATYYCOQFTSS--PFTGSGTKLE	239
QY	237	V 237	
DB	240	I 240	

## RESULT 2

S19663  
Ig lambda chain V region (clone alpha-BSA3) - human

C/Species: Homo sapiens (man)

C/Date: 22-Jan-1993 #sequence\_reviseion 22-Jan-1993 #text\_change 20-Jun-2000

C/Accession: S19663

R/Marke, U.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter

J. Mol. Biol. 222, 581-597, 1991

A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p

A/Reference number: S19663; PMID:92085276; PMID:1748994

A/Accession: S19663  
A/Molecule type: mRNA  
A/Residues: 1-109 <MAR>  
A/Cross-references: EMBL:X61640; NID:g29492; PIDN:CAA4821.1; PID:91340166  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 43.6%; Score 568; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2,2e-32;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SSELTDPAVVALGQTVRITTCQDLSRSTYASWYQKPGQAPVLVYIGKNNRPSGIPDR 190  
Db 1 SSELTDPAVVALGQTVRITTCQDLSRSTYASWYQKPGQAPVLVYIGKNNRPSGIPDR 60

QY 191 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGQTKLTVLG 239  
Db 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGQTKLTVLG 109

## RESULT 3

S47184  
Ig lambda chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C/Accession: S47184  
R/McInosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.  
Submitted to the EMBL Data Library, June 1994  
A/Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient  
A/Reference number: S47181  
A/Accession: S47184  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-108 <MCI>  
A/Cross-references: EMBL:X79783; NID:g506426; PIDN:CAA56179.1; PID:g506427  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 43.1%; Score 562; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 5.5e-32;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SSELTDPAVVALGQTVRITTCQDLSRSTYASWYQKPGQAPVLVYIGKNNRPSGIPDR 190  
Db 1 SSELTDPAVVALGQTVRITTCQDLSRSTYASWYQKPGQAPVLVYIGKNNRPSGIPDR 60

QY 191 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGQTKLTVLG 238  
Db 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGQTKLTVLG 108

## RESULT 4

S41374  
Single chain Fv antibody - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C/Accession: S41374  
R/Atsessenko, O.; Weller, E.W.; Muentz, K.; Conrad, U.  
Submitted to the EMBL Data Library, January 1994  
A/Description: Construction and functional characterization of a single chain Fv antibody  
A/Reference number: S41374  
A/Accession: S41374  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-249 <ART>  
A/Cross-references: EMBL:Z29480

Query Match 43.1%; Score 561.5; DB 2; Length 249;  
Best Local Similarity 48.6%; Pred. No. 1.4e-31;  
Matches 121; Conservative 36; Mismatches 71; Indels 21; Gaps 6;

QY 2 EVOLVESGGGVNPPGSLRLSCAAGSFTEDDYGMGVWRQAPGKGLRWISGIMNGSTGY 61  
Db 1 QVQLQQSGAEIVRPGASVLTCTASGFNPKDYLHVVKQRPKGLRWIARIAPASGNVXY 60

QY 62 ADSVKRFTISDNMKNISLYLQNSLRADPTAVYCAR-----MRAVIMGGGLTVVSRG 117  
Db 61 VPRFDKATITADTSSNTAVYLLSLTSDETVYCARDDTLVTSIGVWGQSTVTVSSR 120

QY 118 GGGSGGGSGGGGSS-ELTQD--PAVSVALGQTVRITTCQ-----GDSLRSYASWYQ 166  
Db 121 GGGSGGGSGGGGSDLELTQSPSVVIRGEVSISCRSKSLTVSDGS-----YLFWFL 176

QY 167 QKPGQAPVLVYIGKNNRPSGIPDRFSGSSGNTASLTITGAQAEDEADYYCNSRDSGNN 226  
Db 177 QKPGQAPVLVYIGKNNRPSGIPDRFSGSSGNTASLTITGAQAEDEADYYCNSRDSGNN 234

QY 227 VPRFGGQTKL 235  
Db 235 LTFGAGTKL 243

## RESULT 5

S36272  
Ig lambda chain V region (clone alpha-THY-29) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C/Accession: S36272  
R/Giffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
EMBO J. 12, 725-734, 1993  
A/Title: Human anti-self antibodies with high specificity from phage display libraries.  
A/Reference number: S36256; MID:93178448; PMID:7679990  
A/Accession: S36272  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-110 <GRI>  
A/Cross-references: EMBL:Z18833; NID:g33419; PIDN:CAA79285.1; PID:g9339912  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 42.3%; Score 551.5; DB 2; Length 110;  
Best Local Similarity 98.2%; Pred. No. 2.9e-31;  
Matches 108; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 131 SSELTDPAVVALGQTVRITTCQDLSRSTYASWYQKPGQAPVLVYIGKNNRPSGIPDR 190  
Db 1 SSELTDPAVVALGQTVRITTCQDLSRSTYASWYQKPGQAPVLVYIGKNNRPSGIPDR 60

QY 191 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGQTKLTVLG 239  
Db 61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGQTKLTVLG 110

## RESULT 6

S70444  
Ig lambda chain precursor V region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C/Accession: S70444; S70426  
R/Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelie, C.  
Mol. Immunol. 29, 1363-1373, 1992  
A/Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of F  
A/Reference number: S70442; MID:93024508; PMID:1383695  
A/Accession: S70444  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-127 <CUI>  
A/Cross-references: UNIPROT:Q9NSD6  
A/Experimental source: clone E29.1  
R/Tonnelie, C.  
Submitted to the EMBL Data Library, May 1990  
A/Reference number: S70426  
A/Accession: S70426

Query Match 42.3%; Score 551.5; DB 2; Length 110;  
Best Local Similarity 98.2%; Pred. No. 2.9e-31;  
Matches 108; Conservative 1; Mismatches 0; Indels 1; Gaps 1;



A;Molecule type: mRNA  
 A;Residues: 1-90 <TON>  
 A;Cross-references: EMBL:X53070  
 A;Experimental source: cell line E29.1, clone VL 29-1  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;1-20/Domain: signal sequence #status predicted <SIG>  
 F;21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>  
 F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 41.9%; Score 546; DB 2; Length 127;  
 Best Local Similarity 97.2%; Pred. No. 8.1e-31;  
 Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 131 SSELTOPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIPDR 190  
 |||||  
 DB 20 SSELTOPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIPDR 79

QY 191 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGKTLTVLG 238  
 |||||  
 DB 80 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGKTLTVLG 127

# RESULT 7

Ig lambda chain - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C;Accession: S38498  
 R;Mark: J.D.; Ouehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S  
 submitted to the EMBL Data Library, June 1993  
 A;Description: Human antibody fragments specific for human blood group antigens from a F  
 A;Reference number: S38498  
 A;Accession: S38498  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-108 <MAR>  
 A;Cross-references: EMBL:Z23035; NID:G414043; PIDN:CAA80570.1; PID:G414044  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;14-88/Domain: immunoglobulin homology <IMM>

Query Match 41.5%; Score 541; DB 2; Length 108;  
 Best Local Similarity 97.2%; Pred. No. 1.5e-30;  
 Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 132 SSELTOPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIPDR 191  
 |||||  
 DB 1 SSELTOPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIPDR 60

QY 192 SSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGKTLTVLG 239  
 |||||  
 DB 61 SSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGKTLTVLG 108

# RESULT 8

Ig lambda chain - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C;Accession: S38496  
 R;Mark: J.D.; Ouehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S  
 submitted to the EMBL Data Library, June 1993  
 A;Description: Human antibody fragments specific for human blood group antigens from a F  
 A;Reference number: S38496  
 A;Accession: S38496  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-109 <MAR>  
 A;Cross-references: EMBL:Z23031; NID:G414039; PIDN:CAA80566.1; PID:G414040  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;15-89/Domain: immunoglobulin homology <IMM>

Query Match 41.4%; Score 539; DB 2; Length 109;  
 Best Local Similarity 93.6%; Pred. No. 2.1e-30;  
 Matches 102; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 131 SSELTOPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIPDR 190  
 |||||  
 DB 1 SSELTOPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIPDR 60

QY 191 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGKTLTVLG 239  
 |||||  
 DB 61 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGKTLTVLG 109

# RESULT 9

Ig lambda chain - human  
 C;Species: Homo sapiens (man)  
 C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C;Accession: S25748  
 R;Comitato, G.; Klobbeck, H.G.  
 Eur. J. Immunol. 21, 1513-1522, 1991  
 A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin la  
 A;Reference number: S16439; MUID:91257162; PMID:1904362  
 A;Accession: S25748  
 A;Status: preliminary; translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-233 <COM>  
 A;Cross-references: EMBL:X57813; NID:G33725; PIDN:CAA0950.1; PID:G33726  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;148-216/Domain: immunoglobulin homology <IMM>

Query Match 40.7%; Score 530; DB 2; Length 233;  
 Best Local Similarity 91.7%; Pred. No. 1.9e-29;  
 Matches 100; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 131 SSELTOPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIPDR 190  
 |||||  
 DB 20 SSELTOPAVSVALGQVTRITTCGDSLSRYASWYQKPGQAPLVLYGKNNRPSGIPDR 79

QY 191 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGKTLTVLG 239  
 |||||  
 DB 80 FSGSSSGNTASLTITGAQAEADADYYCNSRDSGNNHVFPGGKTLTVLG 128

# RESULT 10

Ig lambda chain V-III region (Sh) - human  
 C;Species: Homo sapiens (man)  
 C;Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004  
 C;Accession: A01980  
 R;Tilani, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.  
 J. Biol. Chem. 245, 2171-2176, 1970  
 A;Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The complet  
 A;Reference number: A92057; MUID:70166723; PMID:4909564  
 A;Accession: A01980  
 A;Molecule type: protein  
 A;Residues: 1-108 <TIT>  
 A;Cross-references: UNIPROT:P01714  
 A;Note: the sequence of the C region is also given  
 C;Genetics:  
 A;Gene: IGLV@  
 A;Cross-references: GDB:119342; OMIM:147240  
 A;Map position: 22q11.2-22q11.2  
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kai  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1.  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;14-88/Domain: immunoglobulin homology <IMM>  
 F;21-86/Disulfide bonds: #status experimental

Query Match 40.4%; Score 527; DB 1; Length 108;





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 25, 2005, 20:10:00 ; Search time 127.091 Seconds  
(without alignments)  
991.192 Million cell updates/sec

Title: US-10-029-926D-208  
Perfect score: 1303  
Sequence: 1 MEQVLVSSGGVVRPGSLR.....VFEFGTKLTVLGGGCKAK 246

Scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : UnIProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	758	58.2	240	2	Q65ZC9
2	715	54.9	255	2	Q6KBO5
3	700.5	53.8	248	2	Q65ZG7
4	682.5	52.4	298	2	Q9QYF0
5	636	48.8	244	2	Q65ZC8
6	600	46.0	241	2	Q921A6
7	578	44.4	243	2	Q7TOM2
8	552	42.4	107	2	Q9NSD6
9	550.5	42.2	112	2	Q9HCC1
10	547	42.0	487	2	Q65ZL2
11	530	40.7	233	2	Q6GMW4
12	527	40.4	108	1	LV3A_HUMAN
13	512	39.3	472	2	Q6N0B9
14	510	39.1	499	2	Q8NSK4
15	504	38.7	573	2	Q8MU38
16	498.5	38.3	218	2	Q92S81
17	483	37.1	121	2	Q9UL71
18	476	36.5	470	2	Q6PJ44
19	476	36.5	478	2	Q6PI81
20	476	36.5	606	2	Q6GMW2
21	473	36.3	613	2	Q8MUX1
22	472.5	36.3	597	2	Q96BB9
23	472	36.2	464	2	Q6MZU6
24	470	36.1	113	2	Q9UL90
25	465.5	35.7	473	2	Q6MZV7
26	464	35.6	493	2	Q6GMX2
27	461.5	35.4	475	2	Q9UL91
28	456.5	35.0	478	2	Q6MZU6
29	455	34.9	466	2	Q6IN78
30	452.5	34.7	479	2	Q6MZV6
31	446.5	34.3	116	1	HV3T_HUMAN

32	444.5	34.1	122	1	HV3G_HUMAN
33	444	34.1	116	2	Q9UL93
34	444	34.1	473	2	Q91Z05
35	442.5	34.0	465	2	Q6PC64
36	442	33.9	117	1	HV3C_HUMAN
37	440.5	33.8	494	2	Q96K68
38	438.5	33.7	483	2	Q6MZX9
39	438.5	33.7	494	2	Q6ZW64
40	438.5	33.7	544	2	Q6PJ95
41	438	33.6	479	2	Q91WP5
42	436.5	33.5	118	2	Q9UL72
43	436.5	33.5	475	2	Q6GMW7
44	434	33.3	233	2	Q8TBC9
45	434	33.3	480	2	Q6N094

## ALIGNMENTS

## RESULT 1

ID	Q65ZC9	PRELIMINARY:	PRT:	240 AA.
AC	Q65ZC9;			
DT	25-OCT-2004 (TREMBLrel. 28, Created)			
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)			
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DE	Single-chain Fv (Fragment).			
GN	Name=scFv;			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C1q/7;			
RX	MEDLINE=97362799; Pubmed=9219263;			
RA	Kontermann R.E., Wing M.G., Winter G.;			
RT	"Complement recruitment using bispecific diabodies.";			
RL	Nat. Biotechnol. 15:629-631(1997).			
DR	EMBL; Y13056; CAAT7499.1; -.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG_1like.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; Ig; 2.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00406; IG; 2.			
DR	PROSITE; PSS0835; IG_LIKE; 2.			
FT	NON_TER 1			
FT	NON_TER 240			
SQ	SEQUENCE 240 AA; 25569 MW; FDCPD3645F64B373 CRC64;			

Query Match 58.2%; Score 758; DB 2; Length 240;  
Best local similarity 62.9%; Pred. No. 1,8e-47;  
Matches 151; Conservative 32; Mismatches 51; Indels 6; Gaps 4;

QY	2	EVQLVSSGGVVRPGSLRISCASGFTPDYGMVWRQAPGGLGVSSGNNGSTGY 61
DB	1	QVDLVSSGGVLRVPGSLRISCASGFTFSSYGMHWROAPGGLGVVAIVISDGSKTY 60
QY	62	ADSVKGRFTISRANKSLYLQNNSLRAEDTAVYYCAKMPAPVY--WGQGLTVVSRGGG 119
DB	61	ADSVKGRFTISRANKSLYLQNNSLRAEDTAVYYCARMDGSDLDLPKQKTLTVVSSGGG 120
QY	120	GSGGGSGSGGGGSS-ELTODPA-VSVALGQTVRTTCQDLSRSYYASWYQKPGQAPLVLI 177
DB	121	GSGGGSGSGGGGSDIOMTQSPSTLSASIGDVIITTCASSEGIVYKWLAWYQKPGKAPFLDI 180
QY	178	YGNRRPSSGIPDRFSSSSGNTASLTITGAQAEADADYVNSDSSGNHVPFGGRTLV 237
DB	181	YKASLSLRAPSRFSGSGSTDTFTLTSSLDPPDFATYC--QQYSNYPILTPGGTKLERI 238

RESULT 2

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Q6KB05
ID 06KB05 PRELIMINARY; PRT; 255 AA.
AC 06KB05;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE SCFV B8E5 protein (Fragment).
GN Name=SCFV B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Peter J.C., Mallukat G., Tugler J., Maurice D., Roegel J.C.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ746180; CAG34081.1; -.
DR HSSP; P01837; 1KCR.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IG; 2.
DR PROSITE; PSS0835; IG LIKE; 2.
FT NON TER 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 54.9%; Score 715; DB 2; Length 255;
Best Local Similarity 58.8%; Pred. No. 2.6e-44;
Matches 147; Conservative 33; Mismatches 54; Indels 16; Gaps 6;

QY 2 EVOLVESGGGVAPPGSLRLSCAASGFTPDYGMSTVROAPGKLEWVSGINMGSGTGY 61
DB 1 QVQLQQSGGLVQPGSLKLVSCAASGFTFSYGSWVRQTPDKRLIEWVAITITSGSYTYY 60

QY 62 ADSVKGRTTISRDNKNSLYLQMNLSLRADPTAVVYCARM-----RAPVIMGGTTLTVTS 115
DB 61 PDSVKGRTTISRDNKNTLYLQMSLSKSEDTAVYCARHINRYRDAGFDVWGGGTTLTVS 120

QY 116 RGGGSGGGSGGGSGGSS-ELTQDP-AVSVALGQTVRTTCQ-GDSL-----RSYASWYQQ 167
DB 121 SGGGSGGGSGGGSGGSDIWAQSPSSLSVAGEEVIMSCSSGSLNSRNQKYLAWYQQ 180

QY 168 KPGQAPLVLYGKNNRPSGIPDRPSSGSSGNTASLTITGAQAEADYYCNSRDSGNHV 227
DB 181 KPGQSPKLLIYGASTRESGVDPRTGSGSGTDFTLTISVQAEPLAVYICQNDHS--YPL 238

QY 228 VFGGSGTKLTV 237
DB 239 TFGAGTKLEI 248

RESULT 3
Q6SZ07
ID 06SZ07 PRELIMINARY; PRT; 248 AA.
AC 06SZ07;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE B3 (Fv)-PB40 (Fragment).
GN Name=B3 (Fv)-PB40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RA Brinkmann U., Pai L.H., Fitzgerald D.J., Willingham M., Pastan I.;
RT "B3 (Fv)-PB38DEL, a single-chain immunotoxin that causes complete
regression of a human carcinoma in mice.";

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RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620 (1991).
DR EMBL; S57990; AAB19971.2; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IG; 2.
DR PROSITE; PSS0835; IG LIKE; 2.
FT NON TER 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759BA43E570950 CRC64;

Query Match 53.8%; Score 700.5; DB 2; Length 248;
Best Local Similarity 58.0%; Pred. No. 2.8e-43;
Matches 145; Conservative 32; Mismatches 56; Indels 17; Gaps 6;

QY 1 MEVQLVESGGGVAPPGSLRLSCAASGFTPDYGMSTVROAPGKLEWVSGINMGSGTGY 60
DB 1 MDVQLVESGGGLVQPGSLKLVSCAATSGFTFSYIMTWVRQTPDKRLIEWVAITISNDSSAA 60

QY 61 YADVKGRTTISRDNKNSLYLQMNLSLRADPTAVVYCARMRA-----PVIWGGTTLTVTS 116
DB 61 YSDTVKGRFTISRDNKNTLYLQMSRLKSEDTAVYCARGLAMGAFAYWGGGTTLTVS 120

QY 117 GGGSGGGSGGGSGGSS-ELTQDP-AVSVALGQTVRTTCQ-GDSL-----RSYASWYQQXP 169
DB 121 GGGSGGGSGGGSGGSDVLTQSPSLPVSILGQQAISCRSSQITVHNSNGNTYLEWTLQRP 180

QY 170 GQAPLVLYGKNNRPSGIPDRPSSGSSGNTASLTITGAQAEADYYCNSRDSGNHV-- 227
DB 181 GQSPKLLIYKNSRFGVDPDRSGSGSGTDFTLTKISRVEADLVGYC---FQSGHWPP 236

QY 228 VFGGSGTKLTV 237
DB 237 TFGSGTKLEI 246

RESULT 4
Q9QYF0
ID Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE CN 8 single chain antibody.
GN Name=CN 8 scFv;
OS Synthetic construct.
OC other sequences; artificial sequences.
OX NCBI_TaxID=32630;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183931; Pubmed=10706631; DOI=10.1073/pnas.050582197;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phage display subtraction
RT method.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590 (2000).
DR EMBL; AB036341; BAA88633.1; -.
DR PIR; A33933; A33933.
DR PIR; S19112; S19112.
DR HSSP; P01820; 1A70.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IG; 2.
DR PROSITE; PSS0835; IG LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 52.4%; Score 682.5; DB 2; Length 298;
Best Local Similarity 55.7%; Pred. No. 7e-42;
Matches 137; Conservative 28; Mismatches 64; Indels 17; Gaps 5;

QY 2 EVOLVESGGGVAPPGSLRLSCAASGFTPDYGMSTVROAPGKLEWVSGINMGSGTGY 61
DB 1 QVQLQQSGGLVQPGSLKLVSCAASGFTFSYGSWVRQTPDKRLIEWVAITITSGSYTYY 60

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Db      40 QVTLQOOSGGGLVPGGSLKLSLCAASGSDPSRWYMWVROAPGKGLMEIGIINPDSSTINY 99
QY      62 ADSVKGRFTISRDNANKSLYLQNSLRAEDTAVYYCARM---APVIMGGTLVTYVRGG 118
Db      100 TBSLKDFITISRDNANKSLYLQNSKVRSEDTALYCARASYGHSAVGGGTLVTYVSSGG 159
QY      119 GSGSGGSGGSGGSS-ELTODPA-VSVALGQTVRTTCGDSLRSYASWYQKPGQAPLV 176
Db      160 GSGSGGSGGSGGSDILTQSPASLSASVGETVITTCASGNINHYLAWYQKQKSPQL 219
QY      177 IYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYVCSNRDSSGNH---VVEGG 231
Db      220 VYNAKTLADVPSPRFGSGSGGTQVSLKINSLOPEDFGSYCC-----QGFMTTPYTFGG 272
QY      232 GTKLTV 237
Db      273 GTLEI 278

```

## RESULT 5

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ID      065ZC8      PRELIMINARY;      PRT;      244 AA.
AC      065ZC8;
DT      25-OCT-2004 (TEMBLrel. 28, Created)
DT      25-OCT-2004 (TEMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE      Single-chain Fv (Fragment).
GN      Name=scFv;
OS      Homo sapiens (human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
SQ      SEQUENCE FROM N.A.
MEDLINE=97362799; PubMed=9219263;
RX      Konteiman R.E., Wing M.G., Winter G.;
RT      "Complement recruitment using bispecific diabodies.";
RL      Nat. Biotechnol. 15:629-631(1997).
DR      EMBL: Y13057; CAJ73500.1; -.
DR      InterPro: IPR003599; IG.
DR      InterPro: IPR007110; IG_1like.
DR      InterPro: IPR003596; IG_V.
DR      Pfam: PF00047; IG_2.
DR      SMART: SM00409; IG_2.
DR      SMART: SM00406; IG_2.
DR      PROSITE: PS00835; IG_LIKE; 2.
DR      SMART: SM00406; IG_2.
FT      NON_TER 1
FT      NON_TER 244
SQ      SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

```

```

Query Match      48.8%; Score 636; DB 2; Length 244;
Best Local Similarity 50.8%; Pred. No. 1,4e-38;
Matches 124; Conservative 46; Mismatches 64; Indels 10; Gaps 4;

```

```

QY      2 EVOLVSGGVVPGGSLRLSCAAGFTPDYGMWVROAPGKGLMEVSGINNGSGTGY 61
Db      1 QVTLVSGGSAVVKPFGSDVSKSCASGTFPSDHYMHWKQAPGQGLEMMGWIDPNNGDTRF 60
QY      62 ADSVKGRFTISRDNANKSLYLQNSLRAEDTAVYYCAR---MRAPIVIMGGTLVTVS 115
Db      61 AQFPGKRVITWTRDTISIAAYMEVSRILASDDTAVYYCARREGTSALYGMVWGQGLTVTS 120
QY      116 RGGSGGSGGSGGSS-ELTODPA-VSVALGQTVRTTCGDSLRSYASWYQKPGQAP 173
Db      121 GSGSGGSGGSGGSDIQMTQSPSTLSASIGRVTITTCASBGITYMLAWYQKQKSPKAP 180
QY      174 VLVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYVCSNRDSSGNHVVFGCG 233
Db      181 KFLIYKASLSASGAPSRFSGSGSGTDTLTITSSIQPDFTYTC--QQYNSPLTREGGT 238
QY      234 KLTIV 237
Db      239 KLEI 242

```

## RESULT 6

```

ID      0921A6      PRELIMINARY;      PRT;      241 AA.
AC      0921A6;
DT      01-DEC-2001 (TEMBLrel. 19, Created)
DT      01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT      01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE      Anti-CEA 79 single chain Fv (Fragment).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
SQ      SEQUENCE FROM N.A.
MEDLINE=98170165; PubMed=9509426;
RX      Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA      Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT      "Cloning and characterization of cDNAs encoding VH and VL of a
RT      monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT      generation of a single-chain Fv molecule (scFv).";
RL      Mol. Cells 7:816-819(1997).
DR      EMBL: U88067; AAB48044.1; -.
DR      PIR: S19965; S19965.
DR      PIR: S19967; S19967.
DR      PIR: S19968; S19968.
DR      PIR: S26325; S26325.
DR      HSSP: P01607; 1BMW.
DR      SMART: SM00406; IG_2.
DR      PROSITE: PS00835; IG_LIKE; 2.
FT      NON_TER 1
FT      NON_TER 241
SQ      SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

```

```

Query Match      46.0%; Score 600; DB 2; Length 241;
Best Local Similarity 51.9%; Pred. No. 5,6e-36;
Matches 126; Conservative 34; Mismatches 67; Indels 16; Gaps 6;

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```

QY      2 EVOLVSGGVVPGGSLRLSCAAGFTPDYGMWVROAPGKGLMEVSGINNGSGTGY 61
Db      1 QVTLQOOSGPELKKPGETVAKISCAASGTFPTDYGMWVROAPGKGLKMWGINITYTGEPTY 60
QY      62 ADSVKGRFTISRDNANKSLYLQNSLRAEDTAVYYCAR---MRAPIVIMGGTLVTYVRGG 118
Db      61 ADFKGRFAPFSLSTASTALQINLNKNEDTAVYFCARQDLKTFPDYWGQGTITVYSSGG 120
QY      119 GSGSGGSGGSGGSS-ELTODP-AVSVALGQTVRTTCGDSLRSYASWYQKPGQAP--- 173
Db      121 GSGSGGSGGSGGSDILTQSPSLASLGKVTITTCASQDINKIYAWYQKQKSPRRA 180
QY      174 -VLVYIGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDADYVCSNRDSSGNHVVFGCG 232
Db      181 HTLHIYIQ---PGIPSRFSGSGSGRDYFSSINLEPEDIAITYCLHYD---NLHTFGGG 233
QY      233 TKL 235
Db      234 TKL 236

```

## RESULT 7

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ID      07TOM2      PRELIMINARY;      PRT;      243 AA.
AC      07TOM2;
DT      01-OCT-2003 (TEMBLrel. 25, Created)
DT      01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT      01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE      scFv 6H8 protein (Fragment).
GN      Name=scFv 6H8;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C;
RX MEDLINE=2283226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
RA Peter J.C., Eftekhar P., Billiard P., Wallukat G., Hoebeke J.;
RT "scfv single chain antibody variable fragment as inverse agonist for
   the beta-2 adrenergic receptor."
RL J. Biol. Chem. 278:36740-36747(2003).
DR EMBL; AJ574851; CAE00495.1; -.
DR HSSP; P01751; 1A6W.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG_v.
DR PROSITE; PSS0835; IG_LIKE; 2.
FT NON_TER
SQ SEQUENCE 243 AA; 25976 MW; BEFP64D2DC4F76 CRC64;

Query Match 44.4%; Score 578; DB 2; Length 243;
Best Local Similarity 49.4%; Pred. No. 2.3e-34;
Matches 118; Conservative 37; Mismatches 78; Indels 6; Gaps 4;

QY 2 EVOLVESGGGVPRGSLRLSCAASGFTPDYGMVSRQAPGKGLVWVSGINNGSGTGY 61
DB 1 QVQLQSGSELVRGASVKISCAASGFTFTTMMHWKQKHGQGLEWIGNIYFGSGITNY 60
QY 62 ADSVKGRFTISRDNANKSLYLQNMNLSRAEDTAVYYCAR-MRAPYWGQGLVTVSRGGG 120
DB 61 DEKKNKGILTVDTSSSTAYMHLSSLSDESAVYYCARGRGLDWAGTTLTVSSGGG 120
QY 121 SGGGSGGGGSGS-ELTD-DPAVVALDQYTRITCGDSLRSYASVYQKPGQAPVLVY 178
DB 121 SGGGSGGGGSGSDIQMTSSSFVSILGRVLTITCSEDIYNNRLAWYQKPGNAPRLIS 180
QY 179 GKNNRPSGIDPRFSGSSSGMTASLTITGAQAEADYVYCNRSRSGNHVFGGTXLT 237
DB 181 GATSLTGVPSRPSGSGSKDYLITSLTQEDVATYYCQGYWYSTR--TFGGTKLEI 236

RESULT 8
Q9NSD6 PRELIMINARY; PRT; 107 AA.
AC Q9NSD6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, last annotation update)
DE Homo sapiens This CDS feature is included to show the translation of
   the corresponding V region. Presently translation qualifiers on
   DE V_region features are illegal. (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocyte;
RA Hohmann A.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; I43092; AAA69746.2; -.
DR PIR; S70444; S70444.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IG_v.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 42.4%; Score 552; DB 2; Length 107;
Best Local Similarity 98.1%; Pred. No. 7.2e-33;
Matches 105; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 133 ELTDPAVVALDQYTRITCGDSLRSYASVYQKPGQAPVLVYGNKNNRPSGIDPRFS 192

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DB 1 ELTDPAVVALDQYTRITCGDSLRSYASVYQKPGQAPVLVYGNKNNRPSGIDPRFS 60
QY 193 GSSSGNTASLTITGAQAEADYVYCNRSRSGNHVFGGTXLTVLG 239
DB 61 GSSSGNTASLTITGAQAEADYVYCNRSRSGNHVFGGTXLTVLG 107

RESULT 9
Q9HCCI PRELIMINARY; PRT; 112 AA.
AC Q9HCCI;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE Single chain Fv (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
DR HSSP; P01783; 1IGC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IG_v.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 42.2%; Score 550.5; DB 2; Length 112;
Best Local Similarity 94.6%; Pred. No. 9.8e-33;
Matches 106; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 2 EVOLVESGGGVPRGSLRLSCAASGFTPDYGMVSRQAPGKGLVWVSGINNGSGTGY 61
DB 1 EVOLVESGGGVPRGSLRLSCAASGFTPDYGMVSRQAPGKGLVWVSGINNGSGTGY 60
QY 62 ADSVKGRFTISRDNANKSLYLQNMNLSRAEDTAVYYCAR-MRAPYWGQGLVTVSRGGG 112
DB 61 ADSVKGRFTISRDNANKSLYLQNMNLSRAEDTAVYYCAR-RAYLDVYWGQGLTV 112

RESULT 10
Q65ZL2 PRELIMINARY; PRT; 487 AA.
AC Q65ZL2;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, last annotation update)
DE Fv/M4.
GN Name=M4-IFN- $\epsilon$ tau>;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=96272580; PubMed=8688499;
RA Qi Y., Xiang J.;
RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
   antibody secreted from myeloma cells."
RL Hum. Antibodies Hybridomas 6:161-166(1995).
DR EMBL; S82493; AAB37424.2; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.

```





Best Local Similarity 92.6%; Pred. No. 4.8e-31;  
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 132 SEITOPPAVALAGGVVITTCGDSLSRYASWYQKPGQAPLVLYYGNRRPSGIPDR 191  
DB 1 SEITOPPAVALAGGVVITTCGDSLSRYASWYQKPGQAPLVLYYGNRRPSGIPDR 60  
QY 192 SSSSSGNTASLTITGAOAEADYCNRSRDSGNHVFGGTLVTLG 239  
DB 61 SSSSSGNTASLTITGAOAEADYCNRSRDSGNHVFGGTLVTLG 108

## RESULT 13

ID Q6N089 PRELIMINARY; PRT; 472 AA.  
AC Q6N089;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein DKFZp686P15220.  
GN Name=DKFZp686P15220;  
OS Homo sapiens (human);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP TISSUE=FROM N.A.  
RC TISSUE=Human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oanger A.,  
RU Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BX640627; CAB5781.1; -  
DR HSSP: P01861; IADQ  
DR InterPro: IPR003599; IG.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003597; IG-cl.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_v.  
DR Pfam: PF07654; C1-set; 3.  
DR SMART: SM00409; IG; 2.  
DR SMART: SM00407; IG1; 3.  
DR SMART: SM00406; IG; 1.  
DR PROSITE: PSS0835; IG\_LIKE; 4.  
DR PROSITE: PSS0290; IG\_MHC; UNKNOWN\_2.  
KM Hypothetical protein; IG\_MHC; UNKNOWN\_2.  
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 39.3%; Score 512; DB 2; Length 472;  
Best Local Similarity 48.5%; Pred. No. 3e-29;  
Matches 114; Conservative 19; Mismatches 70; Indels 32; Gaps 5;

QY 2 EVOLVESGGGVNPPGSLRLSCAAGFTPDYKMSWRQAPGKLEWVSGINNGSTGY 61  
DB 20 EVOLVESGGGVNPPGSLRLSCAAGFTPDYKMSWRQAPGKLEWVSGINNGSTGY 79  
QY 62 ADVSKGRFTISRDAKNSLYLQNMNSLAEPYAVYCAR-----RAEPIVINGQTLVT 113  
DB 80 ADVSKGRFTISRDAKNSLYLQNMNSLAEPYAVYCAR-----RAEPIVINGQTLVT 139  
QY 114 VSRGGSGGGGGSGGSSSELTQDPAVSVALGQTVRITTCGDSLSRYASWYQKPGQAP 173  
DB 140 VS-----SASTKGPSVPLAPSSKTSSTGTAALGC---LVKDYFPE-----P 178  
QY 174 VLYYGNRRPSGIPDR-----PDRFGSSSGNTASLTITGAOAEADYCNRSRDSGN 225  
DB 179 VTVSNGALTSVGHVTPPAVLQSSGLYSLSSVTVPSSTIGTQYICNVHKSBN 233

RESULT 14  
Q6N5K4 PRELIMINARY; PRT; 499 AA.  
ID Q6N5K4  
AC Q6N5K4;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE MG22165 protein.  
OS Homo sapiens (human);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP TISSUE=FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins B., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettlemen M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Groomwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smaluk D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP TISSUE=FROM N.A.  
RC TISSUE=Blood;  
RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RL EMBL: BC032249; AAH32249.1; -  
DR HSSP: P01876; IOWO.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003597; IG-cl.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_v.  
DR Pfam: PF07654; C1-set; 2.  
DR Pfam: PF00047; IG; 1.  
DR SMART: SM00406; IG; 1.  
DR PROSITE: PSS0835; IG\_LIKE; 4.  
DR PROSITE: PSS0290; IG\_MHC; UNKNOWN\_1.  
SQ SEQUENCE 499 AA; 53376 MW; 93A5C89582054F32 CRC64;

Query Match 39.1%; Score 510; DB 2; Length 499;  
Best Local Similarity 51.3%; Pred. No. 4.4e-29;  
Matches 120; Conservative 14; Mismatches 42; Indels 58; Gaps 8;

QY 2 EVOLVESGGGVNPPGSLRLSCAAGFTPDYKMSWRQAPGKLEWVSGINNGSTGY 61  
DB 20 EVOLVESGGGVNPPGSLRLSCAAGFTPDYKMSWRQAPGKLEWVSGINNGSTGY 79  
QY 62 ADVSKGRFTISRDAKNSLYLQNMNSLAEPYAVYCAR-----RAEPIVINGQTLVT 113  
DB 80 ADVSKGRFTISRDAKNSLYLQNMNSLAEPYAVYCAR-----RAEPIVINGQTLVT 139  
QY 110 TLTVSRRGGGGGGGGSGGSSSELTQDPAVSVALGQTVRITTCGDSLSRYA 162  
DB 140 TVTVS-----SASPTSPKFPFLSLSTGPDGAVVLAALVQ-----TWGOG 176  
QY 163 SWYQKPE-----QAPVLYYGNRRPSGIPDRFGSSSGNTASLTITGAQ 208  
DB 177 -FFQEBLTVTWSSSGG-----VTANRPPS-----QASGDLVYTTSSQLTLPAPQ 222

RESULT 15  
Q6W038



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GenCore version 5.1.6  
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OM protein - protein search, using bw model

Run on: April 25, 2005, 19:56:06 ; Search time 147.14 Seconds  
(without alignments)  
630.846 Million cell updates/sec

Title: US-10-029-926d-235

Perfect score: 1266  
Sequence: 1 MAEVQLVSGGVRPGSL.....RDSGNHVVGSGTKLTVLG 240

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1266	100.0	266	5	ABG92020 Human ant
2	1266	100.0	277	5	Abg78150 Human Fv
3	1266	100.0	277	5	ABG91841 Human ant
4	1262	99.7	277	8	AD128366 Human scf
5	1257	99.3	246	5	ABG78329 Human Fv
6	1257	99.3	246	5	ABG92026 Human Fv
7	1250	98.7	256	5	ABG78334 Human Fv
8	1250	98.7	256	5	ABG92025 Antibody
9	1242	98.1	277	5	ABG78328 Human Fv
10	1242	98.1	277	5	ABG92019 Human ant
11	1223.5	96.6	278	8	AD128367 Human scf
12	1219.5	96.3	280	8	ADJ57363 P-selecti
13	1218.5	96.2	239	5	ABP44926 Human Bly
14	1218.5	96.2	239	7	ADG95753 Single ch
15	1212.5	95.8	239	5	ABP46027 Human Bly
16	1212.5	95.8	239	7	ADG96854 Single ch
17	1212.5	95.8	280	8	AD128368 Human scf
18	1191.5	94.1	239	5	ABP46004 Human Bly
19	1191.5	94.1	239	7	ADG96831 Single ch
20	1187	93.8	309	5	AAW83322 Single ch
21	1187	93.8	309	5	ABP09603 Antio aci
22	1187	93.8	309	6	ABG74384 Single ch
23	1187	93.8	309	7	ADG98737 Human sin
24	1187	93.8	309	8	AD040446 Human sin
25	1181	93.3	238	3	AAV95198 Anti-Plat

26	1178	93.0	244	6	AAO31136 Human CMO
27	1152.5	91.0	260	5	ABG92023 Antibody
28	1149	90.8	242	8	AD158068 Reg IV-sp
29	1144	90.4	263	5	ABG92024 Antibody
30	1139.5	90.0	239	5	ABP46007 Human Bly
31	1139.5	90.0	239	7	ADG96834 Single ch
32	1133	89.5	244	6	AAO31139 Human CMO
33	1132.5	89.5	239	5	ABP46024 Human Bly
34	1132.5	89.5	239	7	ADG96851 Single ch
35	1131.5	89.4	245	6	AAO31137 Human CMO
36	1131	89.3	252	5	ABP45405 Human Bly
37	1131	89.3	252	7	ADG96232 Single ch
38	1129.5	89.2	243	7	ADG30436 Human GMB
39	1127.5	89.1	243	5	ABP46045 Human Bly
40	1127.5	89.1	243	7	ADG96872 Human Bly
41	1126.5	89.0	239	5	ABP46012 Human Bly
42	1126.5	89.0	239	7	ADG96839 Single ch
43	1121	88.5	242	7	ADG30497 Human GMC
44	1120	88.5	291	8	ADN06989 Human EFG
45	1119	88.4	240	5	ABP46002 Human Bly

## ALIGNMENTS

RESULT 1	ABG92020	standard; protein; 266 AA.
ID	ABG92020	
AC	ABG92020;	
XX		
DT	04-DEC-2002 (first entry)	
XX		
DE	Human antibody fragment #204.	
XX		
KW	Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;	
KW	metastasis; hypervariable region; autoimmune disease; thrombosis;	
KW	restenosis; leukaemia; inflammatory disease; cardiovascular disease;	
KW	myocardial infarction; retinopathic disease; abnormal platelet function;	
KW	sulphated tyrosine-dependent protein-protein interaction.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200253700-A2.	
XX		
PD	11-JUL-2002.	
XX		
PF	31-DEC-2001; 2001WO-US049442.	
XX		
PR	29-DEC-2000; 2000US-00751181.	
PR	29-DEC-2000; 2000US-0258948P.	
XX		
PA	(BIOT-) BIO-TECHNOLOGY GEN CORP.	
PI	Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;	
PI	Seatonch E, Richter T, Amit B, Koepelman L, Peretz T, Levanon A;	
XX	WPI; 2002-674776/72.	
DR		
XX		
PT	Novel isolated epitope present on cancer cells and important in	
PT	physiological phenomena such as cell rolling, metastasis and	
PT	inflammation, for treating autoimmune, inflammatory or cardiovascular	
PT	diseases, and cancer.	
XX		
PS	Disclosure; Page 309-310; Opp; English.	
XX		
CC	The invention relates to an isolated epitope present on cancer cells and	
CC	important in physiological phenomena such as cell rolling, metastasis and	
CC	inflammation, where the epitope is capable of being bound by an antibody,	
CC	its antigen-binding fragment or its complex comprising at least one	
CC	antibody or its binding fragment having a first hypervariable region. The	
CC	epitopes are useful for inhibiting cell rolling, inflammation, autoimmune	
CC	disease, thrombosis, restenosis, metastasis, growth and/or replication of	

CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility  
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
 CC leukemia agents, or for decreasing the number of tumour or leukaemia  
 CC cells in a patient, or in the manufacture of a medicament for the above  
 CC mentioned purposes. The epitopes are useful for diagnosing and treating  
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
 CC diseases, cardiovascular diseases such as myocardial infarction,  
 CC retinopathic diseases and other diseases mediated by abnormal platelet  
 CC function and diseases caused by sulphated tyrosine-dependent protein-  
 CC protein interactions. This sequence represents a human antibody fragment  
 CC of the invention  
 CC XX

SO Sequence 266 AA;

Query Match 100.0%; Score 1266; DB 5; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-81;  
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGVVRRPGSGIRLSCASGTFDDYGMWVRQAQKGLWVSGINMGST 60  
 DB 21 MAEVLVESGGGVVRRPGSGIRLSCASGTFDDYGMWVRQAQKGLWVSGINMGST 80  
 QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCARMRAPVWGQTLTVTSRGG 120  
 DB 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCARMRAPVWGQTLTVTSRGG 140  
 QY 121 GSGGGSGGGGSSSELTDPAVSVALGQTVRITCGDSLRSYSYASWYQKFGQAPVLYIG 180  
 DB 141 GSGGGSGGGGSSSELTDPAVSVALGQTVRITCGDSLRSYSYASWYQKFGQAPVLYIG 200  
 QY 181 KNNRPSGIPDRFSGSSSGNTASLITGAQAEDEADYYCNSRDSGNHVVFGGTKLTVLG 240  
 DB 201 KNNRPSGIPDRFSGSSSGNTASLITGAQAEDEADYYCNSRDSGNHVVFGGTKLTVLG 260

RESULT 2

ABG78150  
 ID ABG78150 standard; protein; 277 AA.

AC ABG78150;  
 XX  
 DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #25.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytosolic;  
 KM disulfide Fv; defv; scfv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

OS Homo sapiens.

XX WO200259264-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US049440.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;

XX DR WPI; 2002-619166/66.

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 PT or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favor of other  
 PT cells.

XX Claim 4; Page 155-156; 232pp; English.

PS The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scfv) or a disulfide Fv (dsfv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention  
 CC XX

SO Sequence 277 AA;

Query Match 100.0%; Score 1266; DB 5; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-81;  
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGVVRRPGSGIRLSCASGTFDDYGMWVRQAQKGLWVSGINMGST 60  
 DB 21 MAEVLVESGGGVVRRPGSGIRLSCASGTFDDYGMWVRQAQKGLWVSGINMGST 80  
 QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCARMRAPVWGQTLTVTSRGG 120  
 DB 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCARMRAPVWGQTLTVTSRGG 140  
 QY 121 GSGGGSGGGGSSSELTDPAVSVALGQTVRITCGDSLRSYSYASWYQKFGQAPVLYIG 180  
 DB 141 GSGGGSGGGGSSSELTDPAVSVALGQTVRITCGDSLRSYSYASWYQKFGQAPVLYIG 200  
 QY 181 KNNRPSGIPDRFSGSSSGNTASLITGAQAEDEADYYCNSRDSGNHVVFGGTKLTVLG 240  
 DB 201 KNNRPSGIPDRFSGSSSGNTASLITGAQAEDEADYYCNSRDSGNHVVFGGTKLTVLG 260

RESULT 3

ABG91841  
 ID ABG91841 standard; protein; 277 AA.

AC ABG91841;

XX DT 04-DEC-2002 (first entry)

DE Human antibody fragment #25.

XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;

KM metastasis; hypervariable region; autoimmune diseases; thrombosis;

KM restenosis; leukaemia; retinopathic disease; cardiovascular disease;

KM myocardial infarction; inflammatory disease; abnormal platelet function;

KM sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.

XX WO200253700-A2.

XX PD 11-JUL-2002.

XX PF 31-DEC-2001; 2001WO-US049442.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 XX PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
 PI Stanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX WPI; 2002-674776/72.  
 DR Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer.  
 XX  
 PS Claim 23; Page 233-234; Opp; English.  
 CC The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility  
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia  
 CC cells in a patient, or in the manufacture of a medicament for the above  
 CC mentioned purposes. The epitopes are useful for diagnosing and treating  
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
 CC diseases, cardiovascular diseases such as myocardial infarction,  
 CC rheumatoid diseases and other diseases mediated by abnormal platelet  
 CC function and diseases caused by sulphated tyrosine-dependent protein-  
 CC protein interactions. This sequence represents a human antibody fragment  
 CC of the invention  
 CC  
 XX  
 SQ Sequence 277 AA;  
 Query Match 100.0%; Score 1266; DB 5; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 9, 5e-81;  
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAEVOLVESGGGVRRPGGSLRLSCAASGFTPDYGMGHWQAQPKGLEWVSGINMGST 60  
 DB 21 MAEVOLVESGGGVRRPGGSLRLSCAASGFTPDYGMGHWQAQPKGLEWVSGINMGST 80  
 QY 61 GYADSVKGRFTISRDNKNSLYLQMNSLRADETAVYVCARRAPVIMGGTTLTVSRGGG 120  
 DB 81 GYADSVKGRFTISRDNKNSLYLQMNSLRADETAVYVCARRAPVIMGGTTLTVSRGGG 140  
 QY 121 GSGGGSGGGGSSSELTQDPAVSVALGQTVRITCGDSLRSYASWYQKFGQAPVLYYG 180  
 DB 141 GSGGGSGGGGSSSELTQDPAVSVALGQTVRITCGDSLRSYASWYQKFGQAPVLYYG 200  
 QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGGTKLTVLG 240  
 DB 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGGTKLTVLG 260  
 RESULT 4  
 ADI28366  
 ID ADI28366 standard; protein: 277 AA.  
 XX ADI28366;  
 AC  
 DT 06-MAY-2004 (first entry)  
 DE Human scFv fragment Y1, binds to platelets.  
 XX Human; antibody; scFv; platelet; drug delivery; cancer; therapy.  
 XX Homo sapiens.  
 OS  
 XX WO2004002528-A1.  
 XX PN  
 XX 08-JAN-2004.  
 XX PD  
 XX

PF 30-JUN-2003; 2003MO-US020604.  
 XX  
 PR 01-JUL-2002; 2002US-00189025.  
 XX  
 PA (SAVI-) SAVIENT PHARM INC.  
 XX  
 PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;  
 XX  
 DR WPI; 2004-099189/10.  
 XX  
 PT Composition comprising an agent and/or antibody or its fragment, useful  
 PT for treating auto-immune disease, thrombosis, restenosis, metastasis, or  
 PT for inhibiting growth and/or replication of tumor cells or leukemia  
 PT cells.  
 XX  
 PS Claim 13; SEQ ID NO 1; 58pp; English.  
 CC  
 CC The present sequence is the protein sequence of human scFv fragment Y1.  
 CC This antibody was identified by screening a human antibody phage library  
 CC that has diversity only in the heavy chain CDR3 regions. Fixed human  
 CC platelets were screened in order to identify antibodies that bind  
 CC platelets. The epitope for Y1 antibody is located between amino acids 272  
 CC and 285 on glycosylated, a subunit of the CD42 complex. Y1 also binds the  
 CC N-terminal of PSGL-1, a receptor for E-, L- and P-selectins, and has a  
 CC high affinity for primary leukaemia cells. The invention relates to  
 CC compositions utilising an agent and an antibody or its fragment. The  
 CC agent is a toxin, radioisotope or pharmaceutical agent such as  
 CC doxorubicin. It is complexed or combined with or conjugated to the  
 CC antibody or its fragment. The agent and/or antibody can be present in the  
 CC composition is a sub-clinical amount, i.e. less than the amount generally  
 CC found to be clinically effective when the agent is administered alone.  
 CC The composition is used in claimed methods of: inhibiting cell rolling,  
 CC inflammation, thrombosis, restenosis, metastasis, the growth and/or  
 CC replication of tumour cells or leukaemia cells, an increase in number of  
 CC tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,  
 CC platelet-platelet and/or cell-platelet complex formation, aggregation or  
 CC adhesion; increasing the mortality rate of tumour or leukaemia cells, the  
 CC susceptibility of disease cells to damage by anti-disease agents, and the  
 CC susceptibility of tumour or leukaemia cells to damage by anti-cancer  
 CC agents; and ameliorating the effects of a disease, preventing a disease,  
 CC treating a disease or inhibiting the progress of a disease.  
 CC  
 XX  
 SQ Sequence 277 AA;  
 Query Match 99.7%; Score 1262; DB 8; Length 277;  
 Best Local Similarity 99.6%; Pred. No. 1, 8e-80;  
 Matches 239; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAEVOLVESGGGVRRPGGSLRLSCAASGFTPDYGMGHWQAQPKGLEWVSGINMGST 60  
 DB 21 MAEVOLVESGGGVRRPGGSLRLSCAASGFTPDYGMGHWQAQPKGLEWVSGINMGST 80  
 QY 61 GYADSVKGRFTISRDNKNSLYLQMNSLRADETAVYVCARRAPVIMGGTTLTVSRGGG 120  
 DB 81 GYADSVKGRFTISRDNKNSLYLQMNSLRADETAVYVCARRAPVIMGGTTLTVSRGGG 140  
 QY 121 GSGGGSGGGGSSSELTQDPAVSVALGQTVRITCGDSLRSYASWYQKFGQAPVLYYG 180  
 DB 141 GSGGGSGGGGSSSELTQDPAVSVALGQTVRITCGDSLRSYASWYQKFGQAPVLYYG 200  
 QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGGTKLTVLG 240  
 DB 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGGTKLTVLG 260  
 RESULT 5  
 ABG78329  
 ID ABG78329 standard; protein: 246 AA.  
 XX ABG78329;  
 AC  
 DT 15-NOV-2002 (first entry)  
 XX  
 XX

DE Human Fv molecule hypervariable region related peptide #204.  
 XX  
 XX Human: Fv molecule; hypervariable region; single chain Fv; cytosolic;  
 KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukemia; adenoma;  
 XX lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukemia.  
 OS Homo sapiens.  
 XX  
 XX MO200259264-A2.  
 PN  
 PD 01-AUG-2002.  
 XX  
 XX 31-DEC-2001; 2001WO-US049440.  
 PF  
 XX 29-DEC-2000; 2000US-00751181.  
 PR  
 XX (BIO-T) BIO-TECHNOLOGY GEN CORP.  
 PA  
 XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;  
 PI Plakshin D, Peretz T;  
 XX WPI; 2002-619166/66.  
 DR  
 XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 PT or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favor of other  
 PT cells.  
 XX  
 XX Disclosure; Page 44-45; 232p; English.  
 PS  
 XX The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments of a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukemia cell is an  
 CC acute myeloid leukemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention  
 CC  
 XX  
 SQ Sequence 246 AA;  
 Query Match 99.3%; Score 1257; DB 5; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-80;  
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 EVOLVESGGGVVPRGGSRLRLSCAAGTFPDYGMWVRQAPGKLEWVSGINNNGSGTGY 62  
 DB 2 EVOLVESGGGVVPRGGSRLRLSCAAGTFPDYGMWVRQAPGKLEWVSGINNNGSGTGY 61  
 QY 63 ADVSKGRFTTISRDNKNSLYLQNNSLRAEDTAVYYCARMPAPVIMGGTLVTVSRGGGGS 122  
 DB 62 ADVSKGRFTTISRDNKNSLYLQNNSLRAEDTAVYYCARMPAPVIMGGTLVTVSRGGGGS 121  
 QY 123 GGGGSGGGSSELTQDPAVSVALGQTVRITCGDLSRLSYASWYQQRPGQAPVLVIYGN 182  
 DB 122 GGGGSGGGSSELTQDPAVSVALGQTVRITCGDLSRLSYASWYQQRPGQAPVLVIYGN 181  
 QY 183 NRPSGIPDRPSGSSSGNTASITTTGAQADEADYYCNSRDSSGNHVVFGGCTKLTIVG 240  
 DB 182 NRPSGIPDRPSGSSSGNTASITTTGAQADEADYYCNSRDSSGNHVVFGGCTKLTIVG 239  
 RESULT 6  
 ABG92026  
 ID ABG92026 standard; protein; 246 AA.  
 XX

AC ABG92026;  
 XX  
 XX 04-DEC-2002 (first entry)  
 DT  
 XX  
 XX Antibody protein #5.  
 DE  
 XX  
 XX Antibody; epitope; cancer; tumour; cell rolling; inflammation;  
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;  
 KM reneosis; leukemia; inflammatory disease; cardiovascular disease;  
 KM myocardial infarction; retinopathic disease; abnormal platelet function;  
 KM sulphated tyrosine-dependent protein-protein interaction.  
 XX  
 XX Unidentified.  
 OS  
 XX  
 XX MO200253700-A2.  
 PN  
 XX 11-UTB-2002.  
 PD  
 XX 31-DEC-2001; 2001WO-US049442.  
 PF  
 XX 29-DEC-2000; 2000US-00751181.  
 PR  
 XX 29-DEC-2000; 2000US-0258948P.  
 XX  
 XX (BIO-T) BIO-TECHNOLOGY GEN CORP.  
 PA  
 XX Lazarovits J, Hagai Y, Plakshin D, Vogel T, Nimrod A, Mar-Haim H;  
 PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;  
 XX WPI; 2002-674776/72.  
 DR  
 XX Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer.  
 XX  
 XX Disclosure; Fig 52; 0pp; English.  
 PS  
 XX The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, reneosis, metastasis, growth and/or replication of  
 CC tumour or leukemia cells, increase in number of tumour or leukemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
 CC mortality of tumour or leukemia cells, for increasing the susceptibility  
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
 CC leukemia agents, or for decreasing the number of tumour or leukemia  
 CC cells in a patient, or in the manufacture of a medicament for the above  
 CC mentioned purposes. The epitopes are useful for diagnosing and treating  
 CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory  
 CC diseases, cardiovascular diseases such as myocardial infarction,  
 CC retinopathic diseases and other diseases mediated by abnormal platelet  
 CC function and diseases caused by sulphated tyrosine-dependent protein-  
 CC protein interactions. This sequence represents an antibody protein of the  
 CC invention  
 CC  
 XX  
 SQ Sequence 246 AA;  
 Query Match 99.3%; Score 1257; DB 5; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-80;  
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 EVOLVESGGGVVPRGGSRLRLSCAAGTFPDYGMWVRQAPGKLEWVSGINNNGSGTGY 62  
 DB 2 EVOLVESGGGVVPRGGSRLRLSCAAGTFPDYGMWVRQAPGKLEWVSGINNNGSGTGY 61  
 QY 63 ADVSKGRFTTISRDNKNSLYLQNNSLRAEDTAVYYCARMPAPVIMGGTLVTVSRGGGGS 122  
 DB 62 ADVSKGRFTTISRDNKNSLYLQNNSLRAEDTAVYYCARMPAPVIMGGTLVTVSRGGGGS 121



QY 123 GGGGSGGGSSSELTQDPAVSVALGQTVRITTCQSDLSRSYASWYQOKPGCAPLVLYYGNK 182  
 DB 122 GGGGSGGGSSSELTQDPAVSVALGQTVRITTCQSDLSRSYASWYQOKPGCAPLVLYYGNK 181  
 QY 183 NRPSGIPDRPSSSGSNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTLTVLG 240  
 DB 182 NRPSGIPDRPSSSGSNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTLTVLG 239

RESULT 7  
 ABG78334  
 ID ABG78334 standard; protein; 256 AA.  
 AC ABG78334;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Human Fv molecule hypervariable region related peptide #209.  
 XX  
 KM Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;  
 KM disulfide Fv; dafv; gcfv; cancer; carcinoma; sarcoma; leukemia; adenoma;  
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200259264-A2.  
 PD 01-AUG-2002.  
 XX  
 PF 31-DEC-2001; 2001WO-US049440.  
 PR 29-DEC-2000; 2000US-00751181.  
 XX  
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Stanton E, Levanon A;  
 PI Plaksin D, Peretz T;  
 XX  
 DR MPI, 2002-619166/66.

XX  
 PS Example 9; Page 90; 232pp; English.

CC The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where  
 CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukemia cell is an  
 CC acute myeloid leukemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention

XX  
 SQ Sequence 256 AA;

Query Match 98.7%; Score 1250; DB 5; Length 256;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-79;  
 Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EVOLVBSGGGVNPPGSGSLRLSCAASGFTFDYGMWVRQAPGKGLVWVGGINNGSGTGY 62  
 DB 2 EVOLVBSGGGVNPPGSGSLRLSCAASGFTFDYGMWVRQAPGKGLVWVGGINNGSGTGY 61

QY 63 ADSVKRFTISRDNANSLYLQNNSLRAEDTAVYCARMPAPYIWGGTLVTVSRGGGS 122  
 DB 62 ADSVKRFTISRDNANSLYLQNNSLRAEDTAVYCARMPAPYIWGGTLVTVSRGGGS 121  
 QY 123 GGGGSGGGSSSELTQDPAVSVALGQTVRITTCQSDLSRSYASWYQOKPGCAPLVLYYGNK 182  
 DB 122 GGGGSGGGSSSELTQDPAVSVALGQTVRITTCQSDLSRSYASWYQOKPGCAPLVLYYGNK 181  
 QY 183 NRPSGIPDRPSSSGSNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTLTVLG 240  
 DB 182 NRPSGIPDRPSSSGSNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGKTLTVLG 239

RESULT 8  
 ABG92025  
 ID ABG92025 standard; protein; 256 AA.  
 AC ABG92025;  
 XX  
 DT 04-DEC-2002 (first entry)  
 XX  
 DE Antibody biotag #1.  
 XX  
 KM Antibody; antibody biotag; cancer; tumour; cell rolling; inflammation;  
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;  
 KM restenosis; leukemia; inflammatory disease; cardiovascular disease;  
 KM myocardial infarction; retinopathic disease; abnormal platelet function;  
 KM sulphated tyrosine-dependent protein-protein interaction.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200253700-A2.  
 PD 11-JUL-2002.  
 XX  
 PF 31-DEC-2001; 2001WO-US049442.  
 PR 29-DEC-2000; 2000US-00751181.  
 PR 29-DEC-2000; 2000US-0258948P.  
 XX  
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
 PI Sanchon E, Richter T, Amit B, Koepman L, Peretz T, Levanon A;  
 XX  
 DR MPI, 2002-674776/72.

XX  
 PS Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer.

XX  
 SQ Disclosure; Fig 51; Opp; English.

CC The invention relates to an isolated epitope present on cancer cells and  
 CC important in physiological phenomena such as cell rolling, metastasis and  
 CC inflammation, where the epitope is capable of being bound by an antibody,  
 CC its antigen-binding fragment or its complex comprising at least one  
 CC antibody or its binding fragment having a first hypervariable region. The  
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
 CC tumour or leukemia cells, increase in number of tumour or leukemia  
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
 CC mortality of tumour or leukemia cells, for increasing the susceptibility  
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
 CC leukemia agents, or for decreasing the number of tumour or leukemia  
 CC cells in a patient, or in the manufacture of a medicament for the above  
 CC mentioned purposes. The epitopes are useful for diagnosing and treating  
 CC diseases such as cancer, leukemia, autoimmune diseases, inflammatory  
 CC retinopathic diseases and other diseases mediated by abnormal platelet  
 CC function and diseases caused by sulphated tyrosine-dependent protein-

CC protein interactions. This sequence represents an antibody biotag used in  
 CC the scope of the invention  
 XX  
 SQ Sequence 256 AA;

Query Match 98.7%; Score 1250; DB 5; Length 256;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-79;  
 Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EVQLVDSGGGVVPPGSLRLSCAASGTPPDYGMQSWRQAPGKLEWVSIGINNNGSTGY 62  
 DB 2 EVQLVESGGGVVPPGSLRLSCAASGTPPDYGMQSWRQAPGKLEWVSIGINNNGSTGY 61  
 QY 63 ADVKVRFTISRDNKAKSLYLQNNSLRAEDTAVYYCARMKAPVIMGGGTLVTVSRGGG 122  
 DB 62 ADVKGRFTISRDNKAKSLYLQNNSLRAEDTAVYYCARMKAPVIMGGGTLVTVSRGGG 121  
 QY 123 GGGGSGGGGSELTPDPAVSVALGQTVRITCGDLSASYASWYQKPGQAPVLYIGKN 182  
 DB 122 GGGGSGGGGSELTPDPAVSVALGQTVRITCGDLSASYASWYQKPGQAPVLYIGKN 181  
 QY 183 NRRSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFGGGTLTVLG 240  
 DB 182 NRRSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFGGGTLTVLG 239

RESULT 9  
 ABG78328 standard; protein; 277 AA.  
 ID ABG78328  
 AC ABG78328;  
 XX  
 DT 15-NOV-2002 (first entry)

DE Human Fv molecule hypervariable region related peptide #203.  
 XX  
 KM Human; Fv molecule; hypervariable region; single chain Fv; cytosolic;  
 KM disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;  
 KM lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

OS Homo sapiens.  
 XX  
 PN WO200259264-A2.  
 PD 01-AUG-2002.

PF 31-DEC-2001; 2001WO-US049440.  
 XX  
 PR 29-DEC-2000; 2000US-00751181.

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 XX  
 PI Hagai Y, Lazarevits J, Guy R, Lipschitz O, Stanton E, Levanon A;  
 PI Plaksin D, Peretz T;  
 XX  
 DR WPI; 2002-619166/66.  
 DR N-PSDB; ABS63384.

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct  
 PT or fragment, or construct of fragment with enhanced binding  
 PT characteristics so as to selectively bind target cell in favor of other  
 PT cells.  
 XX  
 PS Claim 141; Fig 14; 232pp; English.

CC The invention relates to a peptide or polypeptide comprising an Fv  
 CC molecule, a construct or fragments or a construct of a fragment with  
 CC enhanced binding characteristics which selectively and/or specifically  
 CC binds to a target cell in favour of other cells, where binding is  
 CC primarily determined by a first hypervariable region and Fv is a single  
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in  
 CC association with or attached, coupled, combined, linked or fused to a  
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where

CC the medicament has activity against a diseased cell, preferably a cancer  
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,  
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an  
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a  
 CC composition for use in inhibiting the growth of a diseased or cancer  
 CC cell. This sequence represents a human Fv molecule hypervariable region  
 CC related peptide of the invention  
 XX  
 SQ Sequence 277 AA;

Query Match 98.1%; Score 1242; DB 5; Length 277;  
 Best Local Similarity 97.9%; Pred. No. 4.5e-79;  
 Matches 235; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAEVLVDSGGGVVPPGSLRLSCAASGTPPDYGMQSWRQAPGKLEWVSIGINNNGST 60  
 DB 21 MAEVLVDSGGGVVPPGSLRLSCAASGTPPDYGMQSWRQAPGKLEWVSIGINNNGST 80  
 QY 61 GVADSVKGRFTISRDNKAKSLYLQNNSLRAEDTAVYYCARLTHPYFWGGGTLVTVSRGG 120  
 DB 81 GVADSVKGRFTISRDNKAKSLYLQNNSLRAEDTAVYYCARLTHPYFWGGGTLVTVSRGG 140  
 QY 121 GSGGGSGGGGSELTPDPAVSVALGQTVRITCGDLSASYASWYQKPGQAPVLYIG 180  
 DB 141 GSGGGSGGGGSELTPDPAVSVALGQTVRITCGDLSASYASWYQKPGQAPVLYIG 200  
 QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFGGGTLTVLG 240  
 DB 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFGGGTLTVLG 260

RESULT 10  
 ABG92019 standard; protein; 277 AA.  
 ID ABG92019  
 AC ABG92019;  
 XX  
 DT 04-DEC-2002 (first entry)

DE Human antibody fragment #203.  
 XX  
 KM Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;  
 KM metastasis; hypervariable region; autoimmune disease; thrombosis;  
 KM restenosis; leukaemia; inflammatory disease; cardiovascular disease;  
 KM myocardial infarction; retinopathic disease; abnormal platelet function;  
 KM sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.  
 XX  
 PN WO200253700-A2.  
 PD 11-JUL-2002.

PF 31-DEC-2001; 2001WO-US049442.  
 XX  
 PR 29-DEC-2000; 2000US-00751181.

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.  
 XX  
 PI Lazarevits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;  
 PI Stanton E, Richter T, Amit B, Koepman L, Peretz T, Levanon A;  
 XX  
 DR WPI; 2002-674776/72.

PT Novel isolated epitope present on cancer cells and important in  
 PT physiological phenomena such as cell rolling, metastasis and  
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular  
 PT diseases, and cancer.  
 XX  
 PS Claim 23; Page 308-309; Opp; English.

CC The invention relates to an isolated epitope present on cancer cells and

CC important in physiological phenomena such as cell rolling, metastasis and  
CC inflammation, where the epitope is capable of being bound by an antibody,  
CC its antigen-binding fragment or its complex comprising at least one  
CC antibody or its binding fragment having a first hypervariable region. The  
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune  
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of  
CC tumour or leukaemia cells, increase in number of tumour or leukaemia  
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-  
CC platelet and/or cell-platelet adhesion or aggregation, for increasing  
CC mortality of tumour or leukaemia cells, for increasing the susceptibility  
CC of diseased cells to damage by anti-disease, anti-cancer or anti-  
CC leukaemia agents, or for decreasing the number of tumour or leukaemia  
CC cells in a patient, or in the manufacture of a medicament for the above  
CC mentioned purposes. The epitopes are useful for diagnosing and treating  
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory  
CC diseases, cardiovascular diseases such as myocardial infarction,  
CC rheumatoid diseases and other diseases mediated by abnormal platelet  
CC function and diseases caused by sulphated tyrosine-dependent protein-  
CC protein interactions. This sequence represents a human antibody fragment  
CC of the invention  
CC  
XX

SQ Sequence 277 AA;

Query Match 98.1%; Score 1242; DB 5; Length 277;  
Best Local Similarity 97.9%; Pred. No. 4,5e-79;  
Matches 235; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGVRRPGSGIRLSCAASGFTFDDYGMNWRQAPGKLEWVSGINMGST 60  
DB 21 MAEVLVESGGGVRRPGSGIRLSCAASGFTFDDYGMNWRQAPGKLEWVSGINMGST 80  
QY 61 GYADSVKGRFTISRDNKNSLYLQNMNSLRADPTAVVYCARMPAPVIMGGTILVTVSRGG 120  
DB 81 GYADSVKGRFTISRDNKNSLYLQNMNSLRADPTAVVYCARMPAPVIMGGTILVTVSRGG 140  
QY 121 GSGGGSGGGGSSSELTOPPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLYIG 180  
DB 141 GSGGGSGGGGSSSELTOPPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLYIG 200  
QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFVGGGTLTVL 240  
DB 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFVGGGTLTVL 260

RESULT 11

AD128367 standard; protein; 278 AA.

XX AD128367;

DT 06-MAY-2004 (first entry)

DE Human scFv fragment Y17, binds to platelets.

KM Human; antibody; scFv; platelet; drug delivery; cancer; therapy.

OS Homo sapiens.

PN WO2004002528-A1.

PD 08-JAN-2004.

PF 30-JUN-2003; 2003WO-US020604.

PR 01-JUL-2002; 2002US-00189025.

PA (SAVI-) SAVIENT PHARM INC.

PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;

XX WPI; 2004-099189/10.

PT Composition comprising an agent and/or antibody or its fragment, useful

PT for treating auto-immune disease, thrombosis, restenosis, metastasis, or  
PT for inhibiting growth and/or replication of tumor cells or leukemia  
PT cells.

PS Claim 13; SEQ ID NO 2; 58pp; English.

CC The present sequence is the protein sequence of human scFv fragment Y17.  
CC This antibody was identified by screening a human antibody phage library  
CC that has diversity only in the heavy chain CDR3 regions. Fixed human  
CC platelets were screened in order to identify antibodies that bind  
CC platelets. Y17 binds leukaemic cells. The invention relates to  
CC compositions utilising an agent and an antibody or its fragment. The  
CC agent is a toxin, radioisotope or pharmaceutical agent such as  
CC doxorubicin. It is complexed or combined with or conjugated to the  
CC antibody or its fragment. The agent and/or antibody can be present in the  
CC composition as a sub-clinical amount, i.e. less than the amount generally  
CC found to be clinically effective when the agent is administered alone.  
CC The composition is used in claimed methods of: inhibiting cell rolling,  
CC inflammation, thrombosis, restenosis, metastasis, the growth and/or  
CC replication of tumour cells or leukaemia cells, an increase in number of  
CC tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,  
CC platelet-platelet and/or cell-platelet complex formation, aggregation or  
CC adhesion; increasing the mortality rate of tumour or leukaemia cells, the  
CC susceptibility of disease cells to damage by anti-disease agents, and the  
CC susceptibility of tumour or leukaemia cells to damage by anti-cancer  
CC agents; and ameliorating the effects of a disease, preventing a disease,  
CC treating a disease or inhibiting the progress of a disease.

SQ Sequence 278 AA;

Query Match 96.6%; Score 1223.5; DB 8; Length 278;  
Best Local Similarity 97.5%; Pred. No. 9e-78;  
Matches 235; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 MAEVLVESGGGVRRPGSGIRLSCAASGFTFD-DYGMNWRQAPGKLEWVSGINMGSS 59  
DB 21 MAEVLVESGGGVRRPGSGIRLSCAASGFTFDLTHFYFWRQAPGKLEWVSGINMGSS 80  
QY 60 TGYADSVKGRFTISRDNKNSLYLQNMNSLRADPTAVVYCARMPAPVIMGGTILVTVSRGG 119  
DB 81 TGYADSVKGRFTISRDNKNSLYLQNMNSLRADPTAVVYCARMPAPVIMGGTILVTVSRGG 140  
QY 120 GSGGGSGGGGSSSELTOPPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLYIG 179  
DB 141 GSGGGSGGGGSSSELTOPPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLYIG 200  
QY 180 GKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFVGGGTLTVL 239  
DB 201 GKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFVGGGTLTVL 260  
QY 240 G 240  
DB 261 G 261

RESULT 12

ADJ57363 standard; protein; 280 AA.

XX ADJ57363;

DT 06-MAY-2004 (first entry)

DE P-selectin glycoprotein ligand-1-binding scFv antibody fragment L32.

KM P-selectin glycoprotein ligand-1; PSGL-1; antibody; scFv; cytostatic;

KW antiinflammatory; immunosuppressive; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT 53..60 /label= CDR1

FT /note= "Specifically referred to in Claim 2"  
 FT 75. .90  
 FT /label= CDR2  
 FT /note= "Specifically referred to in Claim 2"  
 FT 124. 129  
 FT /label= CDR3  
 FT /note= "Specifically referred to in Claim 2"  
 XX  
 XX WO2004003166-A2.  
 XX  
 XX 08-JAN-2004.  
 XX  
 XX 30-JUN-2003; 2003WO-US020602.  
 XX  
 XX 01-JUL-2002; 2002US-00189032.  
 XX  
 XX (SAVANT-) SAVANT PHARM INC.  
 XX  
 XX Levanon A, Ben-Levy R, Plaksin D, Szanton E, Hagai Y;  
 XX Hoch Mar- Chaim H;  
 XX  
 XX WPI; 2004-203378/19.  
 XX  
 XX Novel antibody or its fragment that binds to an epitope of P-Selectin-  
 PT Glycoprotein Ligand-1, useful for diagnosing/prognosing inflammation,  
 PT infection, auto-immune disease, metastasis, tumor/leukemia cell in  
 PT patient.  
 XX  
 XX Claim 1; SEQ ID NO 1; 106pp; English.  
 XX  
 XX The present sequence is that of an scFv antibody fragment, designated  
 CC L32, that binds P-selectin glycoprotein ligand-1 (PSGL-1). The antibody  
 CC was identified by screening a phage library, which had diversity only in  
 CC the heavy chain CDR3 regions, against a leukemia cell to select specific  
 CC antibodies that recognised leukemia cell surface determinants, wherein  
 CC the specific receptor was not previously known or characterised. The  
 CC invention relates to an antibody or its fragment having the binding  
 CC capabilities of L32. Such antibodies can be used in therapeutic,  
 CC diagnostic, prognostic and staging methods. Pharmaceutical compositions  
 CC comprising such antibodies are used to treat conditions related to:  
 CC inhibiting or treating cell rolling, inflammation, autoimmune disease,  
 CC infection (e.g. HIV infection), metastasis, and growth and/or replication  
 CC of tumour cells; increasing the mortality of tumour cells; inhibiting  
 CC growth and/or replication of tumour cells; inhibiting growth and/or  
 CC replication of leukemia cells; increasing the mortality rate of  
 CC leukemia cells; altering the susceptibility of diseased cells to damage  
 CC by anti-disease agents; increasing the susceptibility of tumour cells to  
 CC damage by anti-cancer agents; increasing the susceptibility of leukemia  
 CC cells to damage by anti-leukemia agents; inhibiting increase in number  
 CC of tumour cells in a patient; decreasing the number of tumour cells in a  
 CC patient; inhibiting increase in number of leukemia cells in a patient;  
 CC and decreasing the number of leukemic cells in a patient. Other methods  
 CC are provided to induce antibody-dependent cell-mediated cytotoxicity or  
 CC stimulate natural killer or T cells using the antibodies. A method of  
 CC purging tumour cells from a patient involves incubating the cells with  
 CC the antibody.  
 XX  
 XX Sequence 280 AA:  
 SQ  
 Query Match 96.3%; Score 1219.5; DB 8; Length 280;  
 Best Local Similarity 96.7%; Pred. No. 1.7e-77;  
 Matches 235; Conservative 0; Mismatches 5; Indels 3; Gaps 1;  
 QY 1 MAEVLVESGGGVVRPGGSLRLTCAASGFTD---DYGMSVVRAPKGLIEWSGIMWG 57  
 DB 21 MAEVLVESGGGVVRPGGSLRLTCAASGFTDLPKVKHMRAPKGLIEWSGIMWG 80  
 QY 58 GSTVYASVYKGRFTISRDNANKNSLYLQNNISLRADTAVVYCARARAVINWGQTLVTVSR 117  
 DB 81 GSTVYASVYKGRFTISRDNANKNSLYLQNNISLRADTAVVYCARARAVINWGQTLVTVSR 140  
 QY 118 GGGSGGGGGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSTYASWYQKPGQAPVLY 177

DB 141 GGGSGGGGGGGSSSELTQDPAVSVALGQTVRITTCGDSLRSTYASWYQKPGQAPVLY 200  
 QY 178 IYKNNRPSGIPDRFSGSSSGNTASTLTITGAQAEADADYYCNSRDSGNHVVFGGTXLT 237  
 DB 201 IYKNNRPSGIPDRFSGSSSGNTASTLTITGAQAEADADYYCNSRDSGNHVVFGGTXLT 260  
 QY 238 VLG 240  
 DB 261 VLG 263  
 RESULT 13  
 ABP44926  
 ID ABP44926 standard; protein, 239 AA.  
 XX  
 XX ABP44926;  
 XX  
 XX 19-AUG-2002 (first entry)  
 XX  
 XX Human Blys binding scFv SEQ ID 937.  
 DE  
 XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200202641-A1.  
 XX  
 XX 10-JAN-2002.  
 XX  
 XX 15-JUN-2001; 2001WO-US019110.  
 XX  
 XX 16-JUN-2000; 2000US-0212210P.  
 XX 17-OCT-2000; 2000US-0240816P.  
 XX 16-MAR-2001; 2001US-0276248P.  
 XX 21-MAR-2001; 2001US-0277379P.  
 XX 25-MAY-2001; 2001US-0293499P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 PI  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 XX  
 XX WPI; 2002-114799/15.  
 XX  
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
 PT diagnosis and treatment of cancers and immune disorders.  
 PT  
 XX Claim 1; Page 1520-1521; 3148pp; English.  
 PS  
 XX This invention describes novel antibodies that immunospecifically bind to  
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention  
 XX  
 XX Sequence 239 AA;  
 SQ

Query Match 96.2%; Score 1218.5; DB 5; Length 239;  
 Best Local Similarity 97.9%; Pred. No. 1.7e-77;  
 Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 3 EVOLVESGGGVAPGSGSLRLSCAASGTFPDYGMWVRQAPGKGLEWVSGINNGSGTGY 62  
 DB 1 EVOLVESGGGVAPGSGSLRLSCAASGTFPDYGMWVRQAPGKGLEWVSGINNGSGTGY 60  
 QY 63 ADSVKGRFTISRDNANKSLYLQWNSLRAEDTAVYYCARRRYALDYWGQGLTVTVSRGGG 121  
 DB 61 ADSVKGRFTISRDNANKSLYLQWNSLRAEDTAVYYCARRRYALDYWGQGLTVTVSRGGG 120  
 QY 122 SGGSGSGGSSSELTQDPAVSVALGQTVRTTCGDSLSRYASWYQKPGQAPVLYYTK 181  
 DB 121 SGGSGSGGSSSELTQDPAVSVALGQTVRTTCGDSLSRYASWYQKPGQAPVLYYTK 180  
 QY 182 NNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSGSHVVFSGGTLYTLG 240  
 DB 181 NNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSGSHVVFSGGTLYTLG 239

RESULT 14  
 ID ADG95753 standard; protein; 239 AA.  
 XX ADG95753;  
 AC ADG95753;

DT 11-MAR-2004 (first entry)  
 XX  
 DE Single chain antibody that immunospecifically binds Blys SeqID 937.  
 XX

KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;  
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;  
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;  
 KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;  
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.  
 XX  
 OS Unidentified.

OS  
 PN WO2003055979-A2.  
 XX  
 PD 10-JUL-2003.  
 XX  
 PF 14-NOV-2002; 2002WO-US036496.  
 XX  
 PR 16-NOV-2001; 2001US-0331469P.  
 PR 19-DEC-2001; 2001US-0340817P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;  
 PI WPI; 2003-505530/47.  
 XX  
 DR Novel antibody that immunospecifically binds to a B lymphocyte stimulator  
 PT (Blys), useful for detecting and treating diseases or disorders e.g.  
 PT rheumatoid arthritis, asthma and leukemia.  
 PT  
 XX

XX Example 1; SEQ ID NO 937; 394dp; English.

CC This invention relates to novel antibodies that immunospecifically bind  
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to  
 CC chromosome 13q34 and encodes a protein that is a member of the tumour  
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
 CC proliferation and differentiation. Specifically, it refers to single  
 CC chain antibody molecules (scFvs) derived, preferably, from the variable  
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
 CC fragment thereof, of either human, murine, rat or monkey Blys. The  
 CC present invention refers to the use of such antibodies in various methods  
 CC for the detection, diagnosis and prognosis of diseases related to the  
 CC aberrant expression or inappropriate function of Blys or its receptor. As  
 CC such, these compositions are useful for identifying immune disorders

CC including myasthenia gravis and multiple sclerosis, inflammatory  
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and  
 CC lymphoma. Accordingly, they can be described as exhibiting various  
 CC activities such as antirheumatic, antiallergic, neuroprotective,  
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This  
 CC polypeptide sequence is a single chain antibody that binds Blys of the  
 CC invention. NOTE: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format  
 CC directly from WIPO at fcp.wipo.int/pub/published pct\_sequences.

XX Sequence 239 AA;

Query Match 96.2%; Score 1218.5; DB 7; Length 239;  
 Best Local Similarity 97.9%; Pred. No. 1.7e-77;  
 Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 3 EVOLVESGGGVAPGSGSLRLSCAASGTFPDYGMWVRQAPGKGLEWVSGINNGSGTGY 62  
 DB 1 EVOLVESGGGVAPGSGSLRLSCAASGTFPDYGMWVRQAPGKGLEWVSGINNGSGTGY 60  
 QY 63 ADSVKGRFTISRDNANKSLYLQWNSLRAEDTAVYYCARRRYALDYWGQGLTVTVSRGGG 121  
 DB 61 ADSVKGRFTISRDNANKSLYLQWNSLRAEDTAVYYCARRRYALDYWGQGLTVTVSRGGG 120  
 QY 122 SGGSGSGGSSSELTQDPAVSVALGQTVRTTCGDSLSRYASWYQKPGQAPVLYYTK 181  
 DB 121 SGGSGSGGSSSELTQDPAVSVALGQTVRTTCGDSLSRYASWYQKPGQAPVLYYTK 180  
 QY 182 NNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSGSHVVFSGGTLYTLG 240  
 DB 181 NNRPSGIPDRFSGSSSGNTASLTITGAQADEADYYCNSRDSGSHVVFSGGTLYTLG 239

RESULT 15  
 ID ABP46027 standard; protein; 239 AA.  
 XX ABP46027;  
 AC ABP46027;

DT 19-AUG-2002 (first entry)  
 XX  
 DE Human Blys binding scFv SEQ ID 2038.

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.  
 XX  
 PN WO200202641-A1.  
 XX

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.  
 XX  
 PR 16-JUN-2000; 2000US-0212210P.  
 PR 17-OCT-2000; 2000US-0240816P.  
 PR 16-MAR-2001; 2001US-0276248P.  
 PR 21-MAR-2001; 2001US-0277379P.  
 PR 25-MAY-2001; 2001US-0293499P.

PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 PI WPI; 2002-114799/15.

CC Antibodies against B Lymphocyte Stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

PS Claim 1; Page 2830-2831; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and actively such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID)) and acquired immunodeficiency syndrome (AIDS)). ABP3399-ABP4728 represent the antibodies and fragments of the antibodies described in the method of the invention

Sequence 239 AA;

Query Match	95.8%	Score 1212.5	DB 5	Length 239
Best Local Similarity	97.5%	Pred. No. 4.5e-77		
Matches 233, Conservative	0	Mismatches 5	Indels 1	Gaps 1

QY 63 ADVYGRFTTISDNANSTLYLQNNSLRAEDTAVYYCARMR-APVIWGQGLTVTVSRGGGG 1211

Db 61 ADVYGRFTTISRDNANSTLYLQNNSLRAEDTAVYYCARRRVYALDYGQGLTVTVSRGGGG 120

QY 122 SGGGSGGGGSSBELTODPAVSVAGQTIVK1TCGGBSLRSTYASWYQOKPQAPVLYLYGK 1811

Db 121 SGGGSGGGGSSBELTODPAVSVAGQTIVK1TCGGBSLRSTYASWYQOKPQAPVLYLYGK 180

QY 182 NNRPGGIPDRFSGSSSGNTASTLTITGAOKEDADYVYCNSSDSSGNTVYFVGGRKLTLYG 240

Db 181 NNRPGGIPDRFSGSSSGNTASTLTITGAOKEDADYVYCNSSDSSGNTVYFVGGRKLTLYG 239

Search completed: April 25, 2005, 20:22:31  
Job time : 148.14 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 20:24:31 ; Search time 36.9845 Seconds  
(without alignments)  
484.413 Million cell updates/sec

Title: US-10-029-926D-235

Perfect score: 1266  
Sequence: 1 MAEVLVSGGIVRRPGSL.....RDSGNHVVGSGTTLVIG 240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1187	93.8	309	3	US-09-079-029-9
2	1105.5	87.3	312	3	US-09-079-029-10
3	1104.5	87.2	280	3	US-09-260-527-1
4	952.5	75.2	278	3	US-09-260-527-3
5	884.5	69.9	310	3	US-09-079-029-11
6	822	64.9	268	4	US-09-976-118-1
7	803	63.4	240	4	US-09-192-854-2
8	791.5	62.5	334	4	US-09-646-028-53
9	791.5	62.5	339	4	US-09-646-028-55
10	791.5	62.5	348	4	US-09-646-028-51
11	783.5	61.9	245	3	US-08-918-148-75
12	780.5	61.7	245	4	US-09-138-091A-73
13	780.5	61.7	245	4	US-08-918-148-76
14	780.5	61.7	245	4	US-09-138-091A-74
15	777.5	61.4	245	4	US-08-918-148-78
16	777.5	61.4	245	4	US-09-138-091A-76
17	756.5	59.8	281	3	US-09-025-7698-178
18	756.5	59.8	281	4	US-09-490-070A-178
19	756.5	59.8	281	4	US-09-490-153-178
20	756.5	59.8	281	4	US-09-490-324-178
21	753	59.5	244	4	US-08-918-148-77
22	753	59.5	244	4	US-09-138-091A-75
23	726.5	57.4	240	1	US-08-488-113B-148
24	726.5	57.4	240	1	US-08-477-484B-148
25	726.5	57.4	240	2	US-08-646-360-148
26	726.5	57.4	240	3	US-08-839-765-148
27	726.5	57.4	240	3	US-09-136-389-148

28	726.5	57.4	240	3	US-09-610-838-148	Sequence 148, App
29	726.5	57.4	240	4	US-09-711-485-148	Sequence 148, App
30	712.5	56.3	284	3	US-08-564-164A-2	Sequence 2, App1
31	711	56.2	255	3	US-09-553-498-8	Sequence 8, App1
32	711	56.2	255	4	US-09-618-869-8	Sequence 8, App1
33	710	56.1	244	3	US-08-918-148-79	Sequence 7, App1
34	710	56.1	244	4	US-09-138-091A-77	Sequence 63, App1
35	709.5	56.0	289	3	US-09-184-658-63	Sequence 63, App1
36	709.5	56.0	289	4	US-09-504-262D-63	Sequence 14, App1
37	708	55.9	301	2	US-08-661-052-14	Sequence 14, App1
38	708	55.9	301	3	US-09-188-082-14	Sequence 14, App1
39	708	55.9	301	3	US-09-364-088-14	Sequence 14, App1
40	708	55.9	301	3	US-09-102-716-14	Sequence 14, App1
41	708	55.9	553	2	US-08-661-052-16	Sequence 16, App1
42	708	55.9	553	3	US-09-188-082-16	Sequence 16, App1
43	708	55.9	553	3	US-09-364-088-16	Sequence 16, App1
44	708	55.9	553	3	US-09-102-716-16	Sequence 16, App1
45	707	55.8	236	2	US-08-190-199A-65	Sequence 65, App1

#### ALIGNMENTS

```
RESULT 1
US-09-079-029-9
; Sequence 9, Application US/09079029
; Patent No. 6342369
;
GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntarapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPacfin (Genentech)
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-079-029-9
Query Match 93.8%; Score 1187; DB 3; Length 309;
Best Local Similarity 92.3%; Pred. No. 1,2e+88;
Matches 227; Conservative 5; Mismatches 8; Indels 6; Gaps 1;
QY 1 MAEVLVSGGIVRRPGSLRSLSCASGFTPDYGMKSWROARFGKLEWVSGINNNGSGT 60
DB 38 MAEVLVSGGIVRRPGSLRSLSCASGFTPDYGMKSWROARFGKLEWVSGINNNGSGT 97
QY 61 GYADVSKGFTTISRDNKNSLYLQNNSLRAEDTAIVYVCARMRAP-----VINGGCTLVLT 114
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Db      98  GYADSVKGRVLTISRDNKNSLYIQMNSLRADPTAVVYCAKILGAGRWYFDLWKGKTVTV 157
QY      115  VSSGGGGGGGGGGGGSSSELTODPAVSVALGQTVITTCQDLSRYSYASWYQKGOAP 174
Db      158  VSSGGGGGGGGGGGGSSSELTODPAVSVALGQTVITTCQDLSRYSYASWYQKGOAP 217
QY      175  VLVIYGNKRRPSSGIPRFGSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEGGT 234
Db      218  VLVIYGNKRRPSSGIPRFGSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEGGT 277
QY      235  KLTVLG 240
Db      278  KLTVLG 283

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## RESULT 2

```

US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntatapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Minipactin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-079-029-10

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Query Match 87.3%; Score 1105.5; DB 3; Length 312;

Best Local Similarity 86.7%; Pred. No. 4.9e-82; Matches 216; Conservative 5; Mismatches 19; Indels 9; Gaps 1;

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QY      1  MAEQVLVESGGGVRRPGGSLRLSCAASGFTFDYDGMSWVQAQPKGLEWYSGINWNGSGT 60
Db      38  MAGQVLVESGGGLVQPGSLRLSCAASGFTFSYWMNWVAQAPKGLEWVANIKQDQSEK 97
QY      61  GYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVVYCAKILGAGRWYFDLWKGKTVTV 111
Db      98  YYVDYVKGKFTISRDNKNSLYIQMNSLRADPTAVVYCAKILGAGRWYFDLWKGKTVTV 157
QY      112  LVVYVSRGGGGGGGGGGSSSELTODPAVSVALGQTVITTCQDLSRYSYASWYQKGOAP 171
Db      158  TVTVVSGGGGGGGGGGGSSSELTODPAVSVALGQTVITTCQDLSRYSYASWYQKGOAP 217

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QY      172  QAPVLVIYGNKRRPSSGIPRFGSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEG 231
Db      218  QAPVLVIYGNKRRPSSGIPRFGSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEG 277
QY      232  GGTKLTVLG 240
Db      278  GGTKLTVLG 286

```

## RESULT 3

```

US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelson, J.D.
; APPLICANT: Willats, W.G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 280
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
; OTHER INFORMATION: phage display library known as the Synthetic scFv
; OTHER INFORMATION: Library (#1) from the Centre for Protein
; OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
; US-09-260-527-1

```

Query Match 87.2%; Score 1104.5; DB 3; Length 280;

Best Local Similarity 86.5%; Pred. No. 5.2e-82; Matches 215; Conservative 10; Mismatches 15; Indels 3; Gaps 2;

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QY      1  MAEQVLVESGGGVRRPGGSLRLSCAASGFTFDYDGMSWVQAQPKGLEWYSGINWNGSGT 58
Db      21  MAEQVLVESGGGLVQPGSLRLSCAASGFTFSYWMNWVAQAPKGLEWVANIKQDQSEK 80
QY      59  STGYADSVKGRFTISRDNKNSLYIQMNSLRADPTAVVYCAKILGAGRWYFDLWKGKTVTV 117
Db      81  TTDYAAPVKGKFTISRDNKNSLYIQMNSLRADPTAVVYCAKILGAGRWYFDLWKGKTVTV 140
QY      118  GGGGGGGGGGGGGSSSELTODPAVSVALGQTVITTCQDLSRYSYASWYQKGOAPVLV 177
Db      141  GGGGGGGGGGGGGSSSELTODPAVSVALGQTVITTCQDLSRYSYASWYQKGOAPVLV 200
QY      178  IYGNKRRPSSGIPRFGSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEGGT 237
Db      201  IYGNKRRPSSGIPRFGSSSGNTASLTITGAQADEADYYCNSRDSGNNHVFEGGT 260
QY      238  VLG 240
Db      261  VLG 263

```

## RESULT 4

```

US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelson, J.D.
; APPLICANT: Willats, W.G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0

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QY 230 FGGGKLTVLG 240  
Db 240 FGTGKTVLVG 250

## RESULT 7

US-09-192-854-2  
; Sequence 2, Application US/09192854  
; Patent No. 6696245  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Greg  
; APPLICANT: Tomlinson, Ian  
; TITLE OF INVENTION: Methods for Selecting Functional Peptides  
; FILE REFERENCE: 3789/72916  
; CURRENT APPLICATION NUMBER: US/09/192,854  
; CURRENT FILING DATE: 1998-11-17  
; EARLIER APPLICATION NUMBER: 60/066,729  
; EARLIER FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-192-854-2

Query Match 63.4%; Score 803; DB 4; Length 240;  
Best Local Similarity 66.2%; Pred. No. 1.2e-57;  
Matches 159; Conservative 27; Mismatches 48; Indels 6; Gaps 4;

QY 3 EVOLVESGGGVPRGSLRLSCAASGFTPDYGMVSRQAPGKGLEWVSGINMGSTGY 62  
1 EVQLVESGGGLVQPGSLRLSCAASGFTFSYAMSWRQAPGKGLEWVSALISGSGSTYY 60  
QY 63 ADVSKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAKRMARAPV-IMGQGLTVTVSRGGG 121  
Db 61 ADVSKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAKSGYAGFDMGQGLTVTVSRGGG 120  
QY 122 GGGGSGGGGSS--ELTQDP-AVSAVALGQTVRITCGDLSRYSYASWYQKPGAPLV 178  
Db 121 GGGGSGGGGSTDIDMTQSPSSLSASVGDRTYITCRASQISSTYLNWYQKPGAPLV 180  
QY 179 YGKNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVFVGGGTLY 238  
Db 181 YAASSLQSGVPSRFGSGSGTDITLTISLQPEDFAITYCQDSISTYEN--TFGGTIVEI 238

## RESULT 8

US-09-646-028-53  
; Sequence 53, Application US/09646028  
; Patent No. 6562347  
; GENERAL INFORMATION:  
; APPLICANT: Kwak, Larry  
; APPLICANT: Biragyn, Arya  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
; FILE REFERENCE: 14014.0316/P  
; CURRENT APPLICATION NUMBER: US/09/646,028  
; CURRENT FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: 60/077,745  
; PRIOR FILING DATE: 1998-03-12  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 53  
; LENGTH: 334  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-53

Query Match 62.5%; Score 791.5; DB 4; Length 334;

Best Local Similarity 64.1%; Pred. No. 1.5e-56;  
Matches 159; Conservative 26; Mismatches 52; Indels 11; Gaps 4;

QY 3 EVOLVESGGGVPRGSLRLSCAASGFTPDYGMVSRQAPGKGLEWVSGINMGSTGY 62  
Db 80 EVQLVESGGGLVQPGSLRLSCAASGFTFSYAMSWRQAPGKGLEWVSALISGSGSTYY 139  
QY 63 ADVSKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAKRMARAPV-IMGQGLTVTVSR 117  
Db 140 ADVSKGRFASRNRSKNTYTLQNNLRPNDAVYFCANNQDGFCLDNMGQGLTVTVSSR 199  
QY 118 GGGGSGGGGSGGGG--SELTQDP-AVSAVALGQTVRITCGDLSR--SYASWYQKPG 171  
Db 200 GGGGSGGGGSGGGGSGQSVLTQPPSVSAAPGQRTVISTGSRNSITGAGYDVWYQKFP 259  
QY 172 QAPLVLYGKNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVF 231  
Db 260 TAPKVLITYSNMNPSPGVDRFSGSKGTSASLAIITGLQEDBGTYYCQCNDSLSGWLFG 319  
QY 232 GGTGLTVL 239  
Db 320 GGTGLTVL 327

## RESULT 9

US-09-646-028-55  
; Sequence 55, Application US/09646028  
; Patent No. 6562347  
; GENERAL INFORMATION:  
; APPLICANT: Kwak, Larry  
; APPLICANT: Biragyn, Arya  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
; FILE REFERENCE: 14014.0316/P  
; CURRENT APPLICATION NUMBER: US/09/646,028  
; CURRENT FILING DATE: 2000-09-12  
; PRIOR APPLICATION NUMBER: 60/077,745  
; PRIOR FILING DATE: 1998-03-12  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 55  
; LENGTH: 339  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-55

Query Match 62.5%; Score 791.5; DB 4; Length 339;  
Best Local Similarity 64.1%; Pred. No. 1.5e-56;  
Matches 159; Conservative 26; Mismatches 52; Indels 11; Gaps 4;

QY 3 EVOLVESGGGVPRGSLRLSCAASGFTPDYGMVSRQAPGKGLEWVSGINMGSTGY 62  
Db 85 EVQLVESGGGLVQPGSLRLSCAASGFTFSYAMSWRQAPGKGLEWVSALISGSGSTYY 144  
QY 63 ADVSKGRFTISRDNANKSLYLQNNSLRAEDTAVYYCAKRMARAPV-IMGQGLTVTVSR 117  
Db 145 ADVSKGRFASRNRSKNTYTLQNNLRPNDAVYFCANNQDGFCLDNMGQGLTVTVSSR 204  
QY 118 GGGGSGGGGSGGGG--SELTQDP-AVSAVALGQTVRITCGDLSR--SYASWYQKPG 171  
Db 205 GGGGSGGGGSGGGGSGQSVLTQPPSVSAAPGQRTVISTGSRNSITGAGYDVWYQKFP 264  
QY 172 QAPLVLYGKNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVF 231  
Db 265 TAPKVLITYSNMNPSPGVDRFSGSKGTSASLAIITGLQEDBGTYYCQCNDSLSGWLFG 324  
QY 232 GGTGLTVL 239  
Db 325 GGTGLTVL 332

Query Match	Similarity	Score	DB	Length
Best Local	Similarity 64.1%	Pred. No. 1,6e-56;		
Matches	Conservative 159;	Mismatches 26;	Indels 11;	Gaps 4
Qy	3	EVQLVESGGGVYRPGQSLRLSCAASGFTTDDYMSAVRQAPGKGLEWYSGINMGSGTGY	62	
Db	94	EVQLLESGGGLVQSGGSLRLSCVSAISLTRESSAIIYVRQAPGKLEWYSGISFGSDITYY	153	
Qy	63	ADVSGRFTISRDNAKNSLYIQNNISLRADETAVYCAKRPAPYI---WGQGLTVTV-SR	117	
Db	154	ADVSGRFSASDINSKNTIYLTQNNNRAPNDIAYIFCAANNQTNFCLDNWGQGLTVYSSR	213	
Qy	118	GGGGSGGGSGGGSGGS---SELTODPAVSVALGQTVRIITCGSDLR---SYASMYQOKPG	171	
Db	214	GGGGSGGGSGGGSGGSOSVLTQPPVSAAPGQRAVITSCGSRSSNTGAGDVVMYOKFPE	273	
Qy	172	QAPVLVYGGKNNRPSGIPDRFGSSSGSNGTASLITTTGAQAEDEADYVCSNRSDSGNHVFG	231	
Db	274	TAPKVLITISNNNRPSGVPRFSGSKGTSAISLAIITGLQLEDEGTYYCQCNDLDSGLRFG	333	
Qy	232	GGTKLTVL	239	
Db	334	GGTKLTVL	341	

Qy	1	MAEVLQVGGGIVRRPGGSLRLSCAASFTEDDYGMSWVROAPGKGLIEWGIMNNGST	60
Db	1	MAEVLQVGGGIVRRPGGSLRLSCAASFTEDDYGMSWVROAPGKGLIEWGIMNNGST	60
Qy	1	MAEVLQVGGGIVRRPGGSLRLSCAASFTEDDYGMSWVROAPGKGLIEWGIMNNGST	60
Db	1	MAEVLQVGGGIVRRPGGSLRLSCAASFTEDDYGMSWVROAPGKGLIEWGIMNNGST	60
Qy	61	GYADSVYKGFPTISRDNANKSLYLQNSLRPAEDTAVYYCARR---APYVGGGLLVTVSR	117
Db	61	YVADSVYKGFPTISRDNANKSLYLQNSLRPAEDTAVYYCARMSGADADIMGGIMTVSS	120
Qy	118	GGGGSGGGSGGGSGSS-ELTQPPA-VSYALQTVRITCGGSLRSYYASWVQKPGQAPV	175
Db	121	GGGGSGGGSGGGSGSDIVYWGSPSTLSASVEDRAVILTRABEGLYHMLAWVQKPGQAPK	180
Qy	176	LVIYGNKNNPSSGIPDRFGSSSGNTASLTITGAQAEDEADYVQNSRDSGNNHVPFGGQTK	235
Db	181	LVIYKKAASSLASGAPSRFGSGSGADFTLTITSLPDDPATYVC--QQYSNVPVTFGGGQTK	238
Qy	236	LTV 238	
Db	239	LEV 241	

Query Match	Best Local Similarity	Score	DB 4	length	245;
Matches	159;	Conservative	28;	Mismatches	49;
				Indels	7;
				Gaps	4
Qy	1	MAEVLVBSGGGVTVPGGSLRLSCAAGFFTPDDYGMKSWROAPGKGLMEVSGIMNMGST	60		
Db	1	MAEVLVBSGGGVTVPGGSLRLSCAAGFFTPDDYGMKSWROAPGKGLMEVSYISSSGSTI	60		
Qy	61	GYADSVKGRFTISRDNKNSLYTLQMNLSRAEDTAVVYCARRR---APYMGQGLVTVSR	117		
Db	61	YYADSVKGRFTISRDNKNTLYTLQMNLSRAEDTAVVYCARSGEDAFLIMGGIMVTVSS	120		
Qy	118	GGGSGGGGSGGGSS--ELTDDPA--VSVALGQTVRITQGDLSLSYASWTVQKRGQAPV	175		
Db	121	GGGSGGGGSGGGSGSDIVMTQSPSTLSASVDRVAITCRABEGITHYLAWVQOKRGKAPK	180		
Qy	176	LVIYKKNRPFGIPDRFGSSSGGTASTITGAQAEADADYYCNSRDSGHHVYVGGGTK	235		
Db	181	LVIYKASLSAGAPSRFGSGSGADFLTITLSLQPDDEATYYC--QQVSNPPLRTGGGTK	238		
Qy	236	LTV 238			
Db	239	LEV 241			

```

US-08-918-148-76
; Sequence 76, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 76
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-76

```

```

Query Match      61.7%; Score 780.5; DB 3; Length 245;
Best Local Similarity 63.5%; Pred. NO. 8.2e-56;
Matches 155; Conservative 31; Mismatches 51; Indels 7; Gaps 4;

```

```

QY 1 MAEVLVESGGGVVPRGSLRLSCAASGFTPDYGMNWVRAQPGKLEWVSGINWNGST 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MAEVLVQSGGGVVGPGGSLSLSCAVSGITLRTYGMHWVRAQPGKLEWVAGISFGRSE 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCARMPAV---IWGGTLVTYVR 117
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 YVADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCARMPAV---IWGGTLVTYVR 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 GGGSGGGSGGGGGSS-ELTQDPA-VSVALGQTVRITCGDLSRSYASWYQKPGQAPV 175
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 GGGSGGGSGGGGGSDIQMTQSPSTLSASIGDRVITTCASSEGIYHMLAWYQKPGKAPK 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 176 LVITGKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGATK 235
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 LLIYKASLASGAPSRFSGSGSDTFTLTISLQPDFAFYTC--QQYSNYPPLTFGGGATK 238
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 236 LTVL 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 239 LEIL 242
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 14
US-09-138-091A-74
; Sequence 74, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: 9491-013-27
; CURRENT APPLICATION NUMBER: US/09/138,091A
; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: US 60/056,736
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: single chain antibody (scFv) fragments
US-09-138-091A-74

```

```

Query Match      61.7%; Score 780.5; DB 4; Length 245;
Best Local Similarity 63.5%; Pred. NO. 8.2e-56;
Matches 155; Conservative 31; Mismatches 51; Indels 7; Gaps 4;

```

```

QY 1 MAEVLVESGGGVVPRGSLRLSCAASGFTPDYGMNWVRAQPGKLEWVSGINWNGST 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MAEVLVQSGGGVVGPGGSLSLSCAVSGITLRTYGMHWVRAQPGKLEWVAGISFGRSE 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCARMPAV---IWGGTLVTYVR 117
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 YVADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCARMPAV---IWGGTLVTYVR 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 GGGSGGGSGGGGGSS-ELTQDPA-VSVALGQTVRITCGDLSRSYASWYQKPGQAPV 175
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 GGGSGGGSGGGGGSDIQMTQSPSTLSASIGDRVITTCASSEGIYHMLAWYQKPGKAPK 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 176 LVITGKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGATK 235
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 LLIYKASLASGAPSRFSGSGSDTFTLTISLQPDFAFYTC--QQYSNYPPLTFGGGATK 238
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 236 LTVL 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 239 LEIL 242
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 15
US-08-918-148-78
; Sequence 78, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 78
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; NAME/KEY: unknown
; LOCATION: 208
; OTHER INFORMATION: unknown amino acid
US-08-918-148-78

```

```

Query Match      61.4%; Score 777.5; DB 3; Length 245;
Best Local Similarity 63.8%; Pred. NO. 1.4e-55;
Matches 155; Conservative 29; Mismatches 52; Indels 7; Gaps 4;

```

```

QY 1 MAEVLVESGGGVVPRGSLRLSCAASGFTPDYGMNWVRAQPGKLEWVSGINWNGST 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MAEVLVQSGGGVVGPGGSLSLSCAVSGITLRTYGMHWVRAQPGKLEWVAGISFGRSE 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCARMPAV---IWGGTLVTYVR 117
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 YVADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCARMPAV---IWGGTLVTYVR 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 GGGSGGGSGGGGGSS-ELTQDPA-VSVALGQTVRITCGDLSRSYASWYQKPGQAPV 175
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 GGGSGGGSGGGGGSKIQMTQSPSTLSASIGDRVITTCASSEGIYHMLAWYQKPGKAPK 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 176 LVITGKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHVPFGGATK 235
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 LLIYKASLASGAPSRFSGSGSDTFTLTISLQPDFAFYTC--QQYSNYPPLTFGGGATK 238
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 236 LTV 238
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 239 LEI 241
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Search completed: April 25, 2005, 21:12:16

Tue Apr 26 17:12:00 2005

Job time : 37.9845 secs

us-10-029-926d-235.ra1

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Page 7

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 20:22:46 ; Search time 106.164 Seconds  
(without alignments)  
752.325 Million cell updates/sec

Title: US-10-029-926D-235

Perfect score: 1266  
Sequence: 1 MAEVLVESGGGVRRPGSL.....RDSGNHVVGGSTKLTVLG 240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: Published Applications AA:  
2: /cgn2\_6/prodata/2/pubppa/US07\_PUBCOMB.pep:\*  
3: /cgn2\_6/prodata/2/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/2/pubppa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/2/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/2/pubppa/PCUTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/prodata/2/pubppa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/2/pubppa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/prodata/2/pubppa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/prodata/2/pubppa/US09C\_PUBCOMB.pep:\*  
11: /cgn2\_6/prodata/2/pubppa/US09C\_NEW\_PUB.pep:\*  
12: /cgn2\_6/prodata/2/pubppa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/prodata/2/pubppa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/prodata/2/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/prodata/2/pubppa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/prodata/2/pubppa/US10C\_PUBCOMB.pep:\*  
17: /cgn2\_6/prodata/2/pubppa/US10C\_NEW\_PUB.pep:\*  
18: /cgn2\_6/prodata/2/pubppa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/prodata/2/pubppa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/prodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1266	100.0	266	US-10-032-037B-204	Sequence 204, App
2	1266	100.0	266	US-10-029-988B-204	Sequence 204, App
3	1266	100.0	266	US-10-032-423A-204	Sequence 204, App
4	1266	100.0	277	US-10-032-037B-25	Sequence 25, App1
5	1266	100.0	277	US-10-029-988B-25	Sequence 25, App1
6	1266	100.0	277	US-10-032-423A-25	Sequence 25, App1
7	1266	100.0	277	US-10-029-926B-25	Sequence 25, App1
8	1242	98.1	277	US-10-032-037B-203	Sequence 203, App
9	1242	98.1	277	US-10-029-988B-203	Sequence 203, App
10	1242	98.1	277	US-10-032-423A-203	Sequence 203, App
11	1242	98.1	277	US-10-029-926B-203	Sequence 203, App
12	1218.5	96.2	239	US-09-880-748-937	Sequence 937, App
13	1218.5	96.2	239	US-10-293-418-937	Sequence 937, App

14	1214.5	95.9	280	US-10-880-922-6	Sequence 6, App1
15	1212.5	95.8	239	US-09-880-748-2038	Sequence 2038, App
16	1212.5	95.8	239	US-10-293-418-2038	Sequence 2038, App
17	1205.5	95.2	280	US-10-880-922-5	Sequence 5, App1
18	1205.5	95.2	280	US-10-880-922-56	Sequence 56, App1
19	1204.5	95.1	280	US-10-880-922-60	Sequence 60, App1
20	1201.5	94.9	280	US-10-880-922-61	Sequence 61, App1
21	1200.5	94.8	280	US-10-880-922-55	Sequence 55, App1
22	1191.5	94.1	239	US-09-880-748-2015	Sequence 2015, App
23	1191.5	94.1	239	US-10-293-418-2015	Sequence 2015, App
24	1187	93.8	309	US-10-052-798-9	Sequence 9, App1
25	1187	93.8	309	US-10-288-917-9	Sequence 9, App1
26	1187	93.8	309	US-10-423-448-9	Sequence 42, App1
27	1178	93.0	244	US-10-322-673-42	Sequence 42, App1
28	1139.5	90.0	239	US-09-880-748-2018	Sequence 2018, App
29	1139.5	90.0	239	US-10-293-418-2018	Sequence 2018, App
30	1133	89.5	244	US-10-322-673-45	Sequence 45, App1
31	1132.5	89.5	239	US-09-880-748-2035	Sequence 2035, App
32	1132.5	89.5	239	US-10-293-418-2035	Sequence 2035, App
33	1131.5	89.4	245	US-10-322-673-43	Sequence 43, App1
34	1131	89.3	252	US-09-880-748-1416	Sequence 1416, App
35	1131	89.3	252	US-10-293-418-1416	Sequence 1416, App
36	1129.5	89.2	243	US-10-935-290-69	Sequence 69, App1
37	1127.5	89.1	243	US-09-880-748-2056	Sequence 2056, App
38	1127.5	89.1	243	US-10-293-418-2056	Sequence 2056, App
39	1126.5	89.0	239	US-09-880-748-2023	Sequence 2023, App
40	1126.5	89.0	239	US-10-293-418-2023	Sequence 2023, App
41	1121	88.5	242	US-10-935-290-130	Sequence 130, App
42	1120	88.5	231	US-10-406-830-6	Sequence 6, App1
43	1119	88.4	240	US-09-880-748-2013	Sequence 2013, App
44	1119	88.4	240	US-10-293-418-2013	Sequence 2013, App
45	1117.5	88.3	247	US-09-880-748-996	Sequence 996, App

#### ALIGNMENTS

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RESULT 1
US-10-032-037B-204
; Sequence 204, Application US/10032037B
; Publication No. US2004001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPTOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-204

Query Match      100.0%; Score 1266; DB 15; Length 266;
Best Local Similarity 100.0%; Pred. No. 38-83;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAEVLVESGGGVRRPGSLRLSCAASGFFEDYIGMSVTRQAQKGLIEWSGINWNGST 60
      |||
DB      21 MAEVLVESGGGVRRPGSLRLSCAASGFFEDYIGMSVTRQAQKGLIEWSGINWNGST 80
      |||
QY      61 GYADSVKGRFTISRDNKNSLYIQNNISLRADPAVYYCAKMRAPVYWGQSTLTVSRGG 120
      |||
DB      81 GYADSVKGRFTISRDNKNSLYIQNNISLRADPAVYYCAKMRAPVYWGQSTLTVSRGG 140
      |||
QY      121 GSGGGSGGGGSELTPDPAVSVALGQTVARITCGDSLRSYASWTQOKRGA PVIYIG 180
      |||
DB      141 GSGGGSGGGGSELTPDPAVSVALGQTVARITCGDSLRSYASWTQOKRGA PVIYIG 200
      |||
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QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 240  
| | | | |  
Db 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 260

RESULT 2  
US-10-029-988B-204  
; Sequence 204, Application US/10029988B  
; Publication No. US20040001839A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/46  
; CURRENT APPLICATION NUMBER: US/10/029, 988B  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 204  
; LENGTH: 266  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-029-988B-204

Query Match 100.0%; Score 1266; DB 15; Length 266;  
Best Local Similarity 100.0%; Pred. No. 3e-83;  
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAEVLVESGGGVVRPGSIRLSCAASGFTFDDYGMWVQAPGKLEWVSGINWNGST 60  
| | | | |  
Db 21 MAEVLVESGGGVVRPGSIRLSCAASGFTFDDYGMWVQAPGKLEWVSGINWNGST 80  
| | | | |  
QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCAKMRAPVIMGGTILTVSRGGG 120  
| | | | |  
Db 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCAKMRAPVIMGGTILTVSRGGG 140  
| | | | |  
QY 121 GSGGGSGGGGSSSELTPDPAVSVALGQTVRITCGDSLRSYASWYQKRGQAPVLVIY 180  
| | | | |  
Db 141 GSGGGSGGGGSSSELTPDPAVSVALGQTVRITCGDSLRSYASWYQKRGQAPVLVIY 200  
| | | | |  
QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 240  
| | | | |  
Db 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 260  
| | | | |

RESULT 3  
US-10-032-423A-204  
; Sequence 204, Application US/10032423A  
; Publication No. US20040002450A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/45  
; CURRENT APPLICATION NUMBER: US/10/032, 423A  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 204  
; LENGTH: 266  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-032-423A-204

Query Match 100.0%; Score 1266; DB 15; Length 266;  
Best Local Similarity 100.0%; Pred. No. 3e-83;  
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGVVRPGSIRLSCAASGFTFDDYGMWVQAPGKLEWVSGINWNGST 60  
| | | | |  
Db 21 MAEVLVESGGGVVRPGSIRLSCAASGFTFDDYGMWVQAPGKLEWVSGINWNGST 80  
| | | | |  
QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCAKMRAPVIMGGTILTVSRGGG 120  
| | | | |  
Db 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCAKMRAPVIMGGTILTVSRGGG 140  
| | | | |  
QY 121 GSGGGSGGGGSSSELTPDPAVSVALGQTVRITCGDSLRSYASWYQKRGQAPVLVIY 180  
| | | | |  
Db 141 GSGGGSGGGGSSSELTPDPAVSVALGQTVRITCGDSLRSYASWYQKRGQAPVLVIY 200  
| | | | |  
QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 240  
| | | | |  
Db 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 260  
| | | | |

RESULT 4  
US-10-032-037B-25  
; Sequence 25, Application US/10032037B  
; Publication No. US20040001822A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/44  
; CURRENT APPLICATION NUMBER: US/10/032, 037B  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 277  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-032-037B-25

Query Match 100.0%; Score 1266; DB 15; Length 277;  
Best Local Similarity 100.0%; Pred. No. 3.1e-83;  
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAEVLVESGGGVVRPGSIRLSCAASGFTFDDYGMWVQAPGKLEWVSGINWNGST 60  
| | | | |  
Db 21 MAEVLVESGGGVVRPGSIRLSCAASGFTFDDYGMWVQAPGKLEWVSGINWNGST 80  
| | | | |  
QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCAKMRAPVIMGGTILTVSRGGG 120  
| | | | |  
Db 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADTAIVYCAKMRAPVIMGGTILTVSRGGG 140  
| | | | |  
QY 121 GSGGGSGGGGSSSELTPDPAVSVALGQTVRITCGDSLRSYASWYQKRGQAPVLVIY 180  
| | | | |  
Db 141 GSGGGSGGGGSSSELTPDPAVSVALGQTVRITCGDSLRSYASWYQKRGQAPVLVIY 200  
| | | | |  
QY 181 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 240  
| | | | |  
Db 201 KNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCNRSRDSGNHVFVGGGKTLVLG 260  
| | | | |

RESULT 5  
US-10-029-988B-25  
; Sequence 25, Application US/10029988B  
; Publication No. US20040001839A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/46  
; CURRENT APPLICATION NUMBER: US/10/029, 988B  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204



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/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 25
/ LENGTH: 277
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-029-988B-25

Query Match      100.0%; Score 1266; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.1e-83;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGVRRPGSLRLSCAASGFTFDDYGMSSWVQAQPKGLEWVSGINWNGST 60
    |||||
DB 21 MAEVLVESGGGVRRPGSLRLSCAASGFTFDDYGMSSWVQAQPKGLEWVSGINWNGST 80
    |||||

QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCARMRAPIVWGQTLTVTSRGGG 120
    |||||
DB 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCARMRAPIVWGQTLTVTSRGGG 140
    |||||

QY 121 GSGGGGGGGGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQOKFGQAPVLVIYG 180
    |||||
DB 141 GSGGGGGGGGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQOKFGQAPVLVIYG 200
    |||||

QY 181 KNNRPGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 240
    |||||
DB 201 KNNRPGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 260
    |||||

RESULT 6
US-10-032-423A-25
/ Sequence 25, Application US/10032423A
/ Publication No. US20040002450A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
/ FILE REFERENCE: 10793/45
/ CURRENT APPLICATION NUMBER: US/10/032,423A
/ PRIOR FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 25
/ LENGTH: 277
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-032-423A-25

Query Match      100.0%; Score 1266; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.1e-83;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGVRRPGSLRLSCAASGFTFDDYGMSSWVQAQPKGLEWVSGINWNGST 60
    |||||
DB 21 MAEVLVESGGGVRRPGSLRLSCAASGFTFDDYGMSSWVQAQPKGLEWVSGINWNGST 80
    |||||

QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCARMRAPIVWGQTLTVTSRGGG 120
    |||||
DB 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCARMRAPIVWGQTLTVTSRGGG 140
    |||||

QY 121 GSGGGGGGGGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQOKFGQAPVLVIYG 180
    |||||
DB 141 GSGGGGGGGGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQOKFGQAPVLVIYG 200
    |||||

QY 181 KNNRPGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 240
    |||||
DB 201 KNNRPGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 260
    |||||

RESULT 7
US-10-029-926B-25
/ Sequence 25, Application US/10029926B
```

```
/ Publication No. US20040073011A1
/ GENERAL INFORMATION:
/ APPLICANT: HAGAY, et al.
/ TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
/ FILE REFERENCE: 10793/50
/ CURRENT APPLICATION NUMBER: US/10/029,926B
/ PRIOR FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 12/29/2000
/ NUMBER OF SEQ ID NOS: 203
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 25
/ LENGTH: 277
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-029-926B-25

Query Match      100.0%; Score 1266; DB 15; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.1e-83;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGVRRPGSLRLSCAASGFTFDDYGMSSWVQAQPKGLEWVSGINWNGST 60
    |||||
DB 21 MAEVLVESGGGVRRPGSLRLSCAASGFTFDDYGMSSWVQAQPKGLEWVSGINWNGST 80
    |||||

QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCARMRAPIVWGQTLTVTSRGGG 120
    |||||
DB 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCARMRAPIVWGQTLTVTSRGGG 140
    |||||

QY 121 GSGGGGGGGGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQOKFGQAPVLVIYG 180
    |||||
DB 141 GSGGGGGGGGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQOKFGQAPVLVIYG 200
    |||||

QY 181 KNNRPGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 240
    |||||
DB 201 KNNRPGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGTKLTVLG 260
    |||||

RESULT 8
US-10-032-037B-203
/ Sequence 203, Application US/10032037B
/ Publication No. US20040001822A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
/ FILE REFERENCE: 10793/44
/ CURRENT APPLICATION NUMBER: US/10/032,037B
/ PRIOR FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 203
/ LENGTH: 277
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-032-037B-203

Query Match      98.1%; Score 1242; DB 15; Length 277;
Best Local Similarity 97.9%; Pred. No. 1.6e-81;
Matches 235; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGVRRPGSLRLSCAASGFTFDDYGMSSWVQAQPKGLEWVSGINWNGST 60
    |||||
DB 21 MAEVLVESGGGVRRPGSLRLSCAASGFTFDDYGMSSWVQAQPKGLEWVSGINWNGST 80
    |||||

QY 61 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCARMRAPIVWGQTLTVTSRGGG 120
    |||||
DB 81 GYADSVKGRFTISRDNKNSLYIQMNSLRADETAVYYCALTHPYFMGQTLTVTSRGGG 140
    |||||

QY 121 GSGGGGGGGGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQOKFGQAPVLVIYG 180
    |||||
DB 141 GSGGGGGGGGSELTPDPVAVSVALGQTVRITCGDSLRSYASWYQOKFGQAPVLVIYG 200
    |||||
```

Db 141 GSGGGGGGGGSELTPDPAVSVALGQTVRITCGDLSRSYASWYQKRGQAPVLVIYG 200  
QY 181 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGKTLTVLG 240  
Db 201 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGKTLTVLG 260

RESULT 9  
US-10-029-988B-203  
; Sequence 203, Application US/10029988B  
; Publication No. US20040001839A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/46  
; CURRENT APPLICATION NUMBER: US/10/029, 988B  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 203  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-029-988B-203

Query Match 98.1%; Score 1242; DB 15; Length 277;  
Best Local Similarity 97.9%; Pred. No. 1.6e-81;  
Matches 235; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MAEVLVESGGGAVRPGGSLRLSCAASGFTFDDYGMWVRQAPGKLEWVSGINMNGST 60  
Db 21 MAEVLVESGGGAVRPGGSLRLSCAASGFTFDDYGMWVRQAPGKLEWVSGINMNGST 80  
QY 61 GYADSVKGRFTISRDNKNSLYLQNMNSLRADTAIVYICARMAPVIMGGSTLTVSRGG 120  
Db 81 GYADSVKGRFTISRDNKNSLYLQNMNSLRADTAIVYICARMAPVIMGGSTLTVSRGG 140  
QY 121 GSGGGGGGGGSELTPDPAVSVALGQTVRITCGDLSRSYASWYQKRGQAPVLVIYG 180  
Db 141 GSGGGGGGGGSELTPDPAVSVALGQTVRITCGDLSRSYASWYQKRGQAPVLVIYG 200  
QY 181 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGKTLTVLG 240  
Db 201 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGKTLTVLG 260

RESULT 10  
US-10-032-423A-203  
; Sequence 203, Application US/10032423A  
; Publication No. US20040002450A1  
; GENERAL INFORMATION:  
; APPLICANT: Bio-Technology General Corp.  
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED  
; FILE REFERENCE: 10793/45  
; CURRENT APPLICATION NUMBER: US/10/032, 423A  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR FILING DATE: 12/29/2000  
; NUMBER OF SEQ ID NOS: 204  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 203  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-423A-203

Query Match 98.1%; Score 1242; DB 15; Length 277;  
Best Local Similarity 97.9%; Pred. No. 1.6e-81;  
Matches 235; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAEVLVESGGGAVRPGGSLRLSCAASGFTFDDYGMWVRQAPGKLEWVSGINMNGST 60  
Db 21 MAEVLVESGGGAVRPGGSLRLSCAASGFTFDDYGMWVRQAPGKLEWVSGINMNGST 80  
QY 61 GYADSVKGRFTISRDNKNSLYLQNMNSLRADTAIVYICARMAPVIMGGSTLTVSRGG 120  
Db 81 GYADSVKGRFTISRDNKNSLYLQNMNSLRADTAIVYICARMAPVIMGGSTLTVSRGG 140  
QY 121 GSGGGGGGGGSELTPDPAVSVALGQTVRITCGDLSRSYASWYQKRGQAPVLVIYG 180  
Db 141 GSGGGGGGGGSELTPDPAVSVALGQTVRITCGDLSRSYASWYQKRGQAPVLVIYG 200  
QY 181 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGKTLTVLG 240  
Db 201 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGKTLTVLG 260

RESULT 11  
US-10-029-926B-203  
; Sequence 203, Application US/10029926B  
; Publication No. US20040073011A1  
; GENERAL INFORMATION:  
; APPLICANT: HUGAT, et al.  
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY  
; FILE REFERENCE: 10793/50  
; CURRENT APPLICATION NUMBER: US/10/029, 926B  
; PRIOR FILING DATE: 2001-12-31  
; PRIOR FILING DATE: 12/29/2000  
; NUMBER OF SEQ ID NOS: 203  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 203  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-029-926B-203

Query Match 98.1%; Score 1242; DB 15; Length 277;  
Best Local Similarity 97.9%; Pred. No. 1.6e-81;  
Matches 235; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MAEVLVESGGGAVRPGGSLRLSCAASGFTFDDYGMWVRQAPGKLEWVSGINMNGST 60  
Db 21 MAEVLVESGGGAVRPGGSLRLSCAASGFTFDDYGMWVRQAPGKLEWVSGINMNGST 80  
QY 61 GYADSVKGRFTISRDNKNSLYLQNMNSLRADTAIVYICARMAPVIMGGSTLTVSRGG 120  
Db 81 GYADSVKGRFTISRDNKNSLYLQNMNSLRADTAIVYICARMAPVIMGGSTLTVSRGG 140  
QY 121 GSGGGGGGGGSELTPDPAVSVALGQTVRITCGDLSRSYASWYQKRGQAPVLVIYG 180  
Db 141 GSGGGGGGGGSELTPDPAVSVALGQTVRITCGDLSRSYASWYQKRGQAPVLVIYG 200  
QY 181 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGKTLTVLG 240  
Db 201 KNNRPSGIDPRFSGSSSGNTASLTITGAQAEADADYYCNSRDSGNHVVFGGKTLTVLG 260

RESULT 12  
US-09-880-748-937  
; Sequence 937, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880, 748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR FILING DATE: 2000-10-17

;; PRIOR APPLICATION NUMBER: 60/276,248  
;; PRIOR FILING DATE: 2001-03-16  
;; PRIOR APPLICATION NUMBER: 60/277,379  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/293,499  
;; PRIOR FILING DATE: 2001-05-25  
;; SOFTWARE: Patent In Ver. 2.0  
;; SEQ ID NO 937  
;; LENGTH: 239  
;; TYPE: PRF  
;; ORGANISM: Homo sapiens  
US-09-880-748-937

Query Match 96.2%; Score 1218.5; DB 10; Length 239;  
Best Local Similarity 97.9%; Pred. No. 6.9e-80;  
Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 3 EVOLVESGGGVNPGGSLRLSCAASGFTPDYGMKSWVROAPGKGLEWVSGINMGSGTGY 62  
|||  
DB 1 EVOLVESGGGVNPGGSLRLSCAASGFTPDYGMKSWVROAPGKGLEWVSGINMGSGTGY 60  
|||  
QY 63 ADSVKGRFTISRDNKNSLYLQNMNLSRAEDTAVYYCARMR-APVINGQGLVTVSRGGG 121  
|||  
DB 61 ADSVKGRFTISRDNKNSLYLQNMNLSRAEDTAVYYCARRRYALDYWGQGLVTVSRGGG 120  
|||  
QY 122 SGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLSRYASWYQOKPGQAPVLYYK 181  
|||  
DB 121 SGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLSRYASWYQOKPGQAPVLYYK 180  
|||  
QY 182 NNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVPFGGTLTVLG 240  
|||  
DB 181 NNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVPFGGTLTVLG 239  
|||

RESULT 13  
US-10-293-418-937  
;; Sequence 937, Application US/10293418  
;; Publication No. US20030223996A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ruden et al.  
;; TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blys  
;; FILE REFERENCE: PFS23P2  
;; CURRENT APPLICATION NUMBER: US/10/293,418  
;; CURRENT FILING DATE: 2002-11-27  
;; PRIOR APPLICATION NUMBER: 60/331,469  
;; PRIOR FILING DATE: 2001-11-16  
;; PRIOR APPLICATION NUMBER: 60/340,817  
;; PRIOR FILING DATE: 2001-12-19  
;; PRIOR APPLICATION NUMBER: 09/880,748  
;; PRIOR FILING DATE: 2001-06-15  
;; PRIOR APPLICATION NUMBER: 60/293,499  
;; PRIOR FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: 60/277,379  
;; PRIOR FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/276,248  
;; PRIOR FILING DATE: 2001-03-16  
;; PRIOR APPLICATION NUMBER: 60/240,816  
;; PRIOR FILING DATE: 2000-10-17  
;; PRIOR APPLICATION NUMBER: 60/212,210  
;; PRIOR FILING DATE: 2000-06-16  
;; NUMBER OF SEQ ID NOS: 3247  
;; SEQ ID NO 937  
;; LENGTH: 239  
;; TYPE: PRF  
;; ORGANISM: Homo sapiens  
US-10-293-418-937

Query Match 96.2%; Score 1218.5; DB 15; Length 239;  
Best Local Similarity 97.9%; Pred. No. 6.9e-80;  
Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 3 EVOLVESGGGVNPGGSLRLSCAASGFTPDYGMKSWVROAPGKGLEWVSGINMGSGTGY 62

DB 1 EVOLVESGGGVNPGGSLRLSCAASGFTPDYGMKSWVROAPGKGLEWVSGINMGSGTGY 60  
|||  
QY 63 ADSVKGRFTISRDNKNSLYLQNMNLSRAEDTAVYYCARMR-APVINGQGLVTVSRGGG 121  
|||  
DB 61 ADSVKGRFTISRDNKNSLYLQNMNLSRAEDTAVYYCARRRYALDYWGQGLVTVSRGGG 120  
|||  
QY 122 SGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLSRYASWYQOKPGQAPVLYYK 181  
|||  
DB 121 SGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLSRYASWYQOKPGQAPVLYYK 180  
|||  
QY 182 NNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVPFGGTLTVLG 240  
|||  
DB 181 NNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVPFGGTLTVLG 239  
|||

RESULT 14  
US-10-880-922-6  
;; Sequence 6, Application US/10880922  
;; Publication No. US2005006955A1  
;; GENERAL INFORMATION:  
;; APPLICANT: PLAKSIN, DANIEL  
;; APPLICANT: LEVANNON, AVIGDOR  
;; APPLICANT: SZANTON, ESTHER  
;; APPLICANT: HAGAY, YOCHVED  
;; APPLICANT: BEN-LEVY, RACHEL  
;; APPLICANT: NISGAV, YAEI  
;; APPLICANT: KANFT, YARIV  
;; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF  
;; FILE REFERENCE: 10793-143  
;; CURRENT APPLICATION NUMBER: US/10/880,922  
;; CURRENT FILING DATE: 2004-06-30  
;; PRIOR APPLICATION NUMBER: 60/484,061  
;; PRIOR FILING DATE: 2003-06-30  
;; NUMBER OF SEQ ID NOS: 64  
;; SOFTWARE: Patent In Ver. 3.2  
;; SEQ ID NO 6  
;; LENGTH: 280  
;; TYPE: PRF  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: consensus antibody  
US-10-880-922-6

Query Match 95.9%; Score 1214.5; DB 17; Length 280;  
Best Local Similarity 96.3%; Pred. No. 1.6e-79;  
Matches 234; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 1 MAEVLVESGGGVNPGGSLRLSCAASGFTPD--DYGMKSWVROAPGKGLEWVSGINMG 57  
|||  
DB 21 MAEVLVESGGGVNPGGSLRLSCAASGFTPDNPVYKHWVROAPGKGLEWVSGINMG 80  
|||  
QY 58 GSTGVADSVKGRFTISRDNKNSLYLQNMNLSRAEDTAVYYCARMR-APVINGQGLVTVSR 117  
|||  
DB 81 GSTGVADSVKGRFTISRDNKNSLYLQNMNLSRAEDTAVYYCARMR-APVINGQGLVTVSR 140  
|||  
QY 118 GGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLSRYASWYQOKPGQAPVLY 177  
|||  
DB 141 GGGGSGGGSSSELTQDPAVSVALGQTVRITTCGDSLSRYASWYQOKPGQAPVLY 200  
|||  
QY 178 IYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVPFGGTLT 237  
|||  
DB 201 IYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADADYYCNSRDSSGNHVPFGGTLT 260  
|||  
QY 238 VLG 240  
|||  
DB 261 VLG 263  
|||

RESULT 15  
US-09-880-748-2038  
;; Sequence 2038, Application US/09880748

```
/ Publication No. US20030059937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ CURRENT FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2038
/ LENGTH: 239
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-880-748-2038

Query Match          95.8%; Score 1212.5; DB 10; Length 239;
Best Local Similarity 97.5%; Pred. No. 1.9e-79;
Matches 233; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY      3  EVLVESGGGVVRPGGSLRLSCAASGFTPDYGMWVRQAPGKGLEWVSGINMGSGSTGY 62
Db      1  EVLVESGGGVVRPGGSLRLSCAASGFTPDYGMWVRQAPGKGLEWVSGINMGSGSTGY 60

QY      63  ADSVKGRFTISRNAKNSLYLQWNSLRAEDTAVYYCARMR-APVINGGTLTVSRGGG 121
Db      61  ADSVKGRFTISRNAKNSLYLQWNSLRAEDTAVYYCARRRYALDYWGQGLTVVSSGGG 120

QY      122  SGGGSGGGSSSETLQDPAVSVALGQTVRIITCGDSLRSYYASWYQKPGQAPLVLYGK 181
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QY      182  NNRPSGIPDRPFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTLTVLG 240
Db      181  NNRPSGIPDRPFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVPFGGTLTVLG 239
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Job time : 107.164 secs